

## FIGURE 1

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGTATG  
AGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACCTGTTAGAAATGTTGGTGGT  
TTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTT  
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGG  
TACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGGCAGTTTTATGCATTG  
CTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAACGTTATCATCAAA  
TTAAACAAGGCTGGCCTTGTACTTGAATACTGAGTTGTTTAGGACTTTCTATTGTGGCAAACCTT  
CCAGAAAACAACCCCTTTTGGCTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCAT  
TATATATGTTTGTTCAGACCATCCTTTCCTACCAAATGCAGCCCAAATCCATGGCAAACAAGTC  
TTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTAGCATGCTGACTTGCTC  
ATCAGTTTTCACAGTGGCAATTTTGGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGG  
ACAAAGGTTATGTGCTTCACATGATCACTACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTT  
GGTTTTTTCCTGACTTACATTTCGTGATTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACA  
TGGATTAACCCCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCA  
GAGATATTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG  
TTCACAGAAGTTGCTTATTCTTCTCTGAAATTTCAACCACCTAATCAAGGCTGACAGTAACACT  
GATGAATGCTGATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCAT  
CAAGAAGACTATTAAAAACACCTATGCCTATACCTTTTTTATCTCAGAAAATAAAGTCAAAAGACT  
ATG

## **FIGURE 2**

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFI~~FSYITAVTLHHIDPALPYISDTGTV~~APEKCLFGAMLNIAAV  
LCIATIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG  
MGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVWCGVSALSMLTCSSVLHSGNFGTDLEQKLHW  
NPEDKGYVLHMITTAAEWSSMSFSFFGFFLT~~YIRDFQKISLRVEANLHGLTLYDTAPCP~~INNERTR  
LLSRDI

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 13-33

#### **Other Transmembrane domains:**

amino acids 54-73, 94-113, 160-180, 122-141

#### **N-myristoylation sites.**

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

### FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACC  
GTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCCTTC  
CTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTTTG  
GATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAG  
GTGATCTTCTCCGTGACGTTTGCATTTTCTTGACCATGTTTGAGCTCATCATCTTTGAAATCTTAGG  
AGTATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGG  
TTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGA  
CTGCTTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCC  
CATTCTCAGCCCAAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTTGGTGTGATTGGAG  
TGACTCTCATGGCTCTTCTTTCTGGATTGGTGCTGTCAACTGCCCATACACTTACATGTCTTACTTC  
CTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGAT  
CATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACA  
AACCATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGGAAGTGAAAATCTTACT  
CTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTTCTGGAAACAGCTGATCT  
ATATGCTACCAAGGAGAGAATAGAACTCCAAAACCTTCAAGGGGAAATATTTAATTTTCTTGTT  
ACTTTTTCTCTATTACTGTGTTTGGAAAATTTTCATGGCTACCATCAATATTGTTTTTGATCGAGTT  
GGGAAAACGGATCCTGTCAAGAGGCATTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGT  
GAAGTTTGGTCCCAACACATTTCTTCATTCTGTTGGAATAATCATCGTCACATCCATCAGAGGAT  
TGCTGATCACTCTTACCAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCATTGTCCTG  
CTATTAGCACAGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCCTT  
AGAATACCGCACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTTG  
ATGTGATCTTCCCTGGTCAGCGCTCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAACAGGCACCA  
GAGAAGCAAATGGCACCTTGAACTTAAAGCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAATTTA  
GATATAAGAGGGGGGAAAAATGGAACCGGGCCTGACATTTTATAAACAAACAAAATGCTATGGTAGC  
ATTTTTACCTTCATAGCATACTCCTTCCCCGTCAGGTGATACTATGACCATGAGTAGCATCAGCCAG  
AACATGAGAGGGGAGAACTAACTCAAGACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGG  
TGTAGAGGCGGAGAGGAGCAAGAACTAAAGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGT  
CTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTTAAGGTTACATGGAAAAGGTTATAGCTTTG  
CCTTGAGATTGACTCATTAAATCAGAGACTGTAACAAAAAAAAAAAAAAAAAAAAAGGCGCGCCGCG  
ACTCTAGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATG

## **FIGURE 4**

MSFLIDSSIMITSQILFFGFWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEILGV  
LNSSSRYPFWKMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTfMYFFWKLGDp  
FPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDILALERRLLQ  
TMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQQEVDAL EELSRO  
LFLETADLYATKERIEYSKTFKGKYNFLGYFFSIYCVWKIFMATINIVFDRVGKTDpVTRGIEI  
TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTkFFyAISSKSSNVIVLLLAQIMGMY  
FVSSVLLIRMSMPLEYRTIITEVLGELQFNfYHRWFDVIFLVSALSSILFLYLAHKQAPeKQMAP

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

#### **N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

#### **Eukaryotic cobalamin-binding proteins**

amino acids 151-160



## FIGURE 5

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGTTCC  
AGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGT  
GTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACT  
TCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGT  
GTCATGCAGAATTATGGGGATCACCCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAG  
AAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCC  
TTGAAAGCTAGCTTTTGAACCTTGACGCTATGGCTGGGTGGAGATGGATTCTGGTTCATCTCTAG  
GATTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCTGATTGGAAGGTTCCAGTGA  
GCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATTCCAGAA  
ATTATCACCACCAAGATCCCATATTCAACACTCAAACGCAACACAAACAGAATTTATGT  
CAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCCCCCTACTACTCTCTC  
CTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTGTGTGCACAGAAGTTTTATG  
GAACTAGCACCATGTCTACAGAACTGAACCATTGTTGAAAATAAGCAGCATTCAAGAATGA  
AGCTGCTGGGTGGTGGAGGTGTCCCCACGGCTCTGCTAGTGTCTGCTCTCTCTCTCTCTCTCTCTG  
CAGCTGGTCTTGGATTTTGTCTATGTCAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAT  
CAGCAGAAGGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCCTAA  
TGAGGAATCAAAGAAAACCTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGC  
GATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTT  
CATGCTCCTTACCCTGCCCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAGAAGAAAGTCCA  
CCCTTGGTTCCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAT  
GCCCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAGCTTCCCACGGCCT  
TTCTAGCCTGGCTATGTCTAATAATATCCCACCTGGGAGAAAGGAGTTTTGCAAAGTGAAGGAC  
CTAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGGTG  
AAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCCGCAGCTCAGACCCCTTCTTCA  
GCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCTTCTGAGCCCGGTAAGAGCAAAAGAAT  
GGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAA  
GCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACTGTGAGCAGGGACTGTAAAC  
ACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACA  
CTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCTAGGAAATATACTTTTACAAGTAACA  
AAAATAAAACTCTTATAAATTTCTATTTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATT  
ACTCAGTAATTTGTTTAAAAAGTAATAAAATTCAACAAACATTTGCTGAATAGCTACTATATGTC  
AAGTGCTGTGCAAGGTATTACACTCTGTAATTGAATATTATTCCTCAAAAAATTGCACATAGTAG  
AACGCTATCTGGGAAGCTATTTTTTTCAGTTTTTGATATTTCTAGCTTATCTACTTCCAACTAAT  
TTTTATTTTTGCTGAGACTAATCTTATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATT  
TATTATTAACATACCTAAGAAGTACATTGTTACCTCTATATACCAAGCACATTTTAAAGTGCC  
ATTAACAAATGTATCACTAGCCCTCCTTTTTTCCAACAAGAAGGACTGAGAGATGCAGAAATATT  
TGTGACAAAAAATTAAGCATTTAGAAAACCTT

## **FIGURE 6**

MARCFSLVLLLTSLIWTTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQQLNFTEAKEACRLLG  
LSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYN  
SSDTWTNSCIPEIIITKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPAPASTSIPR  
RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGFCYVK  
RYVKAFPFTNKNQOKEMIETKVVKEEKANDSNPNEESKKTDKNP EESKSPSKTTVRCLEAEV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

### **Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

### **Tyrosine kinase phosphorylation site.**

amino acids 79-88

### **N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## **FIGURE 7**

CGCCGCGCTCCCGCACCCGCGGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCAGCCCGG  
GGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGCGCCGCGAGCGCAACTCGGTCCAGTCCGGGCGG  
CGGCTGCGGGCGCAGAGCGGAGATGCGAGCGGCTTGGGGCCACCCTGCTGTGCCTGCTGTGGCGG  
CGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTCAAGCCCGGCCG  
GCTCTCAGCTACCCGAGGAGGAGGCCACCTCAATGAGATGTTCCGCGAGGTTGAGGAACTGAT  
GGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGCTA  
AAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCCAGCTATCACAATGAGACCAACACAGAC  
ACGAAGGTTGGAATAATACCATCCATGTGCACCGAGAAATTACAAGATAACCAACAACAGAC  
TGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTGTGGGAGACGAAGAAGGCAGAAGGAGCC  
ACGAGTGCATCATCGACGAGGACTGTGGGCCCAGCATGTACTGCCAGTTTGGCCAGTTCCAGTAC  
ACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAAGTGTGTGGAGACCA  
GCTGTGTGTCTGGGGTCACTGCACCAAAATGGCCACCAGGGGCAGCAATGGGACCATCTGTGACA  
ACCAGAGGGACTGCCAGCCGGGGCTGTGCTGTGCCTTCCAGAGAGGCTGCTGTTCCCTGTGTGC  
ACACCCCTGCCCCGTGGAGGGCGAGCTTGGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCAC  
CTGGGAGCTAGAGCCTGATGGAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGC  
CCACAGCCACAGCCTGGTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGG  
GAGATCCTGCTGCCAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCG  
CCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCCGCTG  
CCGCCGCTGCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAA  
TAGAAATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCTTA  
CATCTTCTTCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCAATTTGTTAGCT  
CCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGTCTGGGAGAGTCAGGCAGGGTTAACTGCA  
GGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAGACAGCCG  
TTTGTCTCATATGGCTTTGATAATTGTTTGGGGGAGGAGATGGAACAATGTGGAGTCTCCCTC  
TGATTGGTTTTGGGAAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAACCTGGCAAAATG  
CAACAAATGAATTTCCACGCAGTTCTTCCATGGGCATAGGTAAGCTGTGCCTTCAGCTGTGTC  
AGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTTATTTCATCCAGCAGTGTGCTCAGCTCC  
TACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTCCCTCTCTCAGCACAGCCTGGGG  
AGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTTGCC  
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCATCTGGTTGTGACTCTAAGCTCAGTGCTCT  
CTCCACTACCCACACAGCCTTGGTGCCACCAAAAGTGCTCCCCAAAAGGAAGGAGAATGGGAT  
TTTTCTTGAGGCATGCACATCTGGAATTAAGGTCAAATAATTCTCACATCCCTCTAAAAGTAAA  
CTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGGCAGCCGTCCTTCTAATGAAGACAATGAT  
ATTGACACTGTCCCTCTTTGGCAGTTGCATTAGTAACCTTTGAAAGGTATATGACTGAGCGTAGCA  
TACAGGTTAACCTGCAGAAACAGTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGC  
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACGTGGAGAAAAATCAAACCGAGCAGGGC  
TGTGTGAAACATGTTTGTAAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATG  
TTTTCAGGTGTCATGGACTGTTGCCACCATGTATTCATCCAGAGTTCTTAAAGTTTAAAGTTGCA  
CATGATTGTATAAGCATGCTTTCTTTGAGTTTAAATTATGTATAAACATAAGTTGCATTTAGAA  
ATCAAGCATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 8**

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQHL  
RSERVEEAEAAAKASSEVNLANLPSPYHNETNTDTKVGNNITIVHREIHKITNNQTGMVFSE  
TVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQMLCTRDSECCGDQLCVWGH  
TKMATRGSNGTICDNQRDCQPLCCAFQRLFFVCTPLPVEGELCHDPASRLDLITWELEPDG  
ALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEVGSFMEEVRQELEDLE  
RSLTEEMALGEPAAAAAALLGGEI

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

### **Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

### **N-myristoylation site.**

amino acids 202-208, 217-223

### **Amidation site.**

amino acids 140-144

## FIGURE 9

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCCAC  
GGCCACCTTGTGAACCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCATCAAAG  
GCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTGGGGCTCTTCTGGACCTT  
AACTGGGTACTGGCCCTGGGCCAATGCGTCTCGCTGGAGCCTTTGCCTCCTTCTACTGGGCCTT  
CCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCCGCACACTCCGTTACC  
ACACTGGGTCATTGGCATTGAGAGCCCTCATCTGACCCTTGTGCAGATAGCCCCGGGTCATCTTG  
GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCTGTAGCCCGCTGCATCATGTGCTGTTT  
CAAGTGTGCTCTGGTGTCTGGAAAAATTTATCAAGTTCCTAAACGCAATGCATACATCATGA  
TCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAAAATGCGTTCATGCTACTCATGCGAAAC  
ATTGTCAGGGTGGTCGTCCTGGACAAAAGTCACAGACCTGCTGCTGTTCTTTGGGAAGCTGCTGGT  
GGTCGGAGGCGTGGGGGCTCTGTCTTCTTTTTTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAG  
ACTTTAAGAGCCCCACCTCAACTATTACTGGCTGCCATCATGACCTCCATCCTGGGGGCCTAT  
GTCATCGCCAGCGGCTTCTTCAGCGTTTTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCCT  
GGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAA  
AGATTCTGGGCAAGAAGAACGAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGAAGCTCCGG  
CCCTGATCCAGGACTGCACCCACCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGT  
CTCCATTTTGTGGTAAAAAAGGTTTTAGGCCAGGCGCGGTGGCTCACGCCTGTAATCCAACACT  
TTGAGAGGCTGAGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTG  
AAACCTCCGTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCTATCCCA  
GCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGA  
GATCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA  
AAGATTTTATTAAAGATATTTTGTAACTC

## **FIGURE 10**

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLEFWTL  
NWVLALGQCVLGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL  
EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAKNAFMLLMRN  
IVRVVLDKVTDLLLFFGKLLVGGVGVLSTFFFSGRIPGLGKDFKSPHLNYYWLPIMTSLGAY  
VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLKILGKKNEAPPDNKKRKK

### **Important features:**

#### **Transmembrane domains:**

amino acids 57-80 (type II), 110-126, 215-231, 254-274

#### **N-glycosylation sites.**

amino acids 16-20, 27-31, 289-293

#### **Hypothetical YBR002c family proteins.**

amino acids 276-288

#### **Ammonium transporters proteins.**

amino acids 204-231

#### **N-myristoylation sites.**

amino acids 60-66, 78-84

#### **Amidation site.**

amino acids 306-310



## **FIGURE 12**

MGACLGACSLLSASCCLGSA PCILSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVESQL  
YKLPWVCEEAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRDPRAAIQ  
NGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFLILQLVLLIDFAHSWNQRWLKAE  
ECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVCSIAAVLPKV  
QDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI  
VGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVAACEGRAFDNEQDGVITYSY  
SFFHFCLVLASLHVMTLTNWKPGETRMISTWTAVVVKICASWAGLLLYLWTLVAPLLLRNRD  
FS

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444



### FIGURE 13

CGGGCCAGCCTGGGGCGGCCGGCCAGGAACCAACCGTTAAGGTGTCTTCTCTTTAGGGATGGTGA  
GGTTGGAAAAAGACTCCTGTAACCCCTCCTCCAGGATGAACCACTGCCAGAAGACATGGAGAACG  
CTCTCACCGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCACACAA  
CTCATGGCCAGGATTGAGTCCTATGAAGGAAGGAAAAGAAAGGCATATCTGATGTCAGGAGGAC  
TTTCTGTTTGTGTGTACCTTTGACCTCTTATTCGTAACATTACTGTGGATAATAGAGTTAAATG  
TGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTACTATTCTTCATAT  
TTTGATATATTTCTTCTGGCAGTTTTTCGATTTAAAGTGTTAATACTTGCCATATGCTGTGTGCAG  
ACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCCTTTTTACTAGCAAAAG  
TGATCCTTTTGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTGCCCATCATTTTCATTCATC  
CTTGCCCTGGATTGAGACGTGGTTCCCTGGATTTCAAAGTGTTACCTCAAGAAGCAGAAGAAGAAAA  
CAGACTCCTGATAGTTCAGGATGCTTCAGAGAGGGCAGCACCTTATACCTGGTGGTCTTTCTGATG  
GTCAGTTTTATTCCCTCCTGAATCCGAAGCAGGATCTGAAGAAGCTGAAGAAAAACAGGACAGT  
GAGAAACCACTTTTAGAACTATGAGTACTACTTTTGTTAAATGTGAAAAACCTCACAGAAAGTC  
ATCGAGGCAAAAAGAGGCAGGCAGTGGAGTCTCCCTGTGACAGTAAAGTTGAAATGGTGACGTC  
CACTGCTGGCTTTATTGAACAGCTAATAAAGATTTATTTATTGTAATACCTCACAAACGTTGTAC  
CATATCCATGCACATTTAGTTGCCCTGCCTGTGGCTGGTAAGGTAATGTCATGATTCATCCTCTCT  
TCAGTGAGACTGAGCCTGATGTGTTAACAAATAGGTGAAGAAAGTCTTGCTGTATTCCCTAATC  
AAAAGACTTAATATATTGAAGTAACACTTTTTTTAGTAAGCAAGATACCTTTTTATTTCATTCAC  
AGAATGGAATTTTTTTGTTTCATGTCTCAGATTTATTTGTATTTCTTTTTTAACACTCTACATT  
TCCCTTGTTTTTTAACTCATGCACATGTGCTCTTTGTACAGTTTTAAAAAGTGAATAAAATCTG  
ACATGTCAATGTGGCTAGTTTTATTTTCTTGTTTTGCATTATGTGTATGGCCTGAAGTGTGGA  
CTTGCAAAAGGGGAAGAAAGGAATTGCGAATACATGTAAATGTCACCAGACATTTGTATTATTT  
TTATCATGAAATCATGTTTTTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTGAATGC  
ACAAATGACTTAAACCATTATATCATGTTTCCTTTGCGTTCAGCCAATTTCAATTAAATGAA  
CTAAATTAAAAA

## **FIGURE 14**

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLF  
VTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTT  
AVTSAFLLAKVILSKLFSQGAFGYVLPPIISFILAWIETWFLDFKVLQPQAEENRLLIVQDASER  
AALIPGGLSDGQFYSPPESEAGSEEAEKQDSEKPLLEL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domains:**

amino acids 54-72, 100-118, 130-144, 146-166

**N-myristoylation sites.**

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

## FIGURE 15

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGACTGAGG  
 CCGCGGCTGCCCCGCGGCTCCCTGCGCCGCCGCTCCCGGGACAGAAGATGCTGCTCCAG  
 GGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGACGGGTGCCCAT  
 CCGGCTGCCAGTGCCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGGACACGGTGCCC  
 CGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGC  
 AGGCAGCTTTGCCGGCTGCCGGGCTGCAGTCTTGGACCTGTCACAGAACCAGATCGCCAGCC  
 TGCCAGCGGGGTCTCCAGCCACTCGCCAACCTCAGCAACCTGGACCTGACGGCCAACAGGCTG  
 CATGAAATCACCAATGAGACCTTCCGTGGCTGCGGCGCTCGAGCGCTCTACCTGGGCAAGAA  
 CCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGCTCGACCGCTCCTGGAGCTCAAGCTGC  
 AGGACAACGAGCTGCGGGCACTGCCCCGCTGCGCTGCCCGCTGCTGCTGCTGGACCTCAGC  
 CACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACCTGGAGGCGCTGCGGCT  
 GGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACC  
 TGGATGTGTCCGACAACAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCTCCGGGGCTGACG  
 CGCTTGGCTGGCCGGCAACACCCGCTTGGCCAGCTGCGGCGCGAGGACCTGGCCGGCTGGC  
 TGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCTGCTGGCGACCTCTCGGGCC  
 TCTTCCCCGCTGCGGCTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCTTGAGC  
 TGGTTTGGCCCTGGGTGCGCGAGAGCCACGTCACTAGGCCAGCCCTGAGGAGACGCGTGCCA  
 CTTCCCGCCCAAGAAGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCAG  
 CCACCACCACAGCCACAGTGCCACCACGAGGCGCGTGGTGCGGGAGCCACAGCCTTGCTCT  
 TCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCGGCCACTGAGGCCCCAGCCCGCCTC  
 CACTGCCCCACCGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCCTCCACCTGCCTCA  
 ATGGGGGCACATGCCACCTGGGGACACGGCACCCCTGGCGTGCTTGTGCCCCGAAGGCTTCAG  
 GGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACAGTCACGCCGAG  
 GCCACCACGGTCCCTGACCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGC  
 AGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCG  
 GGCCCTGATAAGCGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACAGGTCACCCA  
 GCTGCGGCCCCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGGCCCGGGCGGGTGCCCGAGG  
 GCGAGGAGGCTGCGGGGAGGCCCATACACCCAGCCGTCCACTCCAACCACGCCCCAGTCACC  
 CAGGCCCCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCTGGCCGCGGTGCTCCTGGCCGC  
 GCTGGCTGCGGTGGGGGAGCCTACTGTGTGCGGCGGGGGCGGGCCATGGCAGCAGCGGCTCAGG  
 ACAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAAGTGGAGGGAGTGAAGGTCCCCTTGAG  
 CCAGGCCCAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCC  
 ACTCATGGGCTTCCAGGGCTGGCTCCAGTCACCCCTCCACGCAAGCCCTACATCTAAGCCA  
 GAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCC  
 ACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGACAGAGGGCTGTGTGACCACAGCT  
 GGGCCCTGTCCCTCTGGACCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCC  
 CTAACGTCCCCAGAACCAGTGCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTC  
 CCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGTCTGCTGGGCTCTCCAC  
 TCCAGGCGGACCCTGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGC  
 GGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAGAACTGGAAGGAAGATGC  
 TTTAGGAACATGTTTTGCTTTTTTAAATATATATTTATAAGAGATCCTTTCCCATTTATTCT  
 GGAAGATGTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAGACAAACGATGATATGAA  
 GCCTTTTGTAGAAAAAATAAAGATGAAGTGTGAAA

## **FIGURE 16**

MCSRVPILLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPRDPVPPDTVGLYVFENGIT  
MLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLRRLERLY  
LGKNRIRHIQPGAFDTLDRLELKLQDNELRALPPLRLPRLLLLDLSHNSLLALEPGILDTANVE  
ALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDL  
AGLAALQELDVSNSLSLQALPGDLSGLFPRLRLAAARNPFNCVPLSWFGPWVRESHVTIASPEE  
TRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAP  
SPPSTAPPTVGPVPQPDCCPSTCLNGGTCHLGRHHLACLCEGFTGLYCESQMGQGRPSPTP  
VTPRPPRSLTLGIEPVSPSLRVGLQRYLQGSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEY  
TVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAV  
LLAALAAVGAAYCVRGRAMAAAAQDKGQVGPAGPLELEGVKVPLEPGPKATEGGGEALPSGSE  
CEVPLMGFPGLQSPHAKPYI

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 579-599

#### **EGF-like domain cysteine pattern signature.**

amino acids 430-442

#### **Leucine zipper pattern.**

amino acids 197-219, 269-291

#### **N-glycosylation sites.**

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

#### **Tyrosine kinase phosphorylation sites.**

amino acids 124-131, 337-345

#### **N-myristoylation sites.**

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,  
594-600, 640-646

## FIGURE 17

GCAGCGGCGAGGCGGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCATGCG  
GGTCCGGATAGGGCTGACGCTGCTGCTGTGTGCGGTGCTGCTGAGCTTGGCCTCGGCGTCTCGG  
ATGAAGAAGGCAGCCAGGATGAATCCTTAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTA  
AAGGACCATACTACTGCAGGCAGAGTAGTTGCTGGTCAAATATTTCTTGATTGAGAAGAATCTGA  
ATTAGAATCCTCTATTCAAGAAGAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAGTGTACAG  
AAGATATCAGCTTTCTAGAGTCTCCAAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTA  
CGGAAACCAGCTTTGACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCT  
TTTCTAGATAAGGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTG  
CTACAACCTATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAACTGAAGAAGAGGCTGCT  
AAGAGACGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGAATGAAAATCCTTAATGGAAG  
CAATAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAGGCAGCAAGCATGAACCATA  
CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTTGGTGATTACTTGCCACAGAATATCCAG  
GCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGCTCTTGG  
CTTTCTGTATGCCTCTGGACTTGGTGTAAATCAAGTCAGGCAAAGGCTCTTGTATATTATACAT  
TTGGAGCTCTTGGGGCAATCTAATAGCCACATGGTTTTGGTAAGTAGACTTAGTGAAGGCT  
AATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACCTTTTTCAGCTTTCATGATC  
CAGATTTGCTTGTATTAAGACCAAATATTCAGTTGAACTTCCTTCAAATCCTTGTAAATGGATAT  
AACACATGGAATCTACATGTAAATGAAAGTTGGTGGAGTCCACAATTTTTCTTTAAATGATTAG  
TTTGGCTGATTGCCCCAAAAAGAGAGATCTGATAAATGGCTCTTTTAAATTTTCTCTGAGTTG  
GAATTGTCAGAATCATTTTTTACATTAGATTATCATAATTTTAAAAATTTTCTTTAGTTTTTCA  
AAATTTTGTAAATGGTGGCTATAGAAAAACAACATGAAATATTATACAATATTTGCAACAATGC  
CCTAAGAATTGTTAAATTCATGGAGTTATTTGTGCAGAATGACTCCAGAGAGCTCTACTTTCTG  
TTTTTTACTTTTCATGATTGGCTGTCTTCCATTTATTCTGGTCATTTATTGCTAGTGACACTGT  
GCCTGCTTCCAGTAGTCTCATTTTCCCTATTTTGCTAATTTGTTACTTTTTCTTTGCTAATTTGG  
AAGATTAATCATTTTTTAATAAATTTATGTCTAAGATTAAAAAAAAAAAAAAAAAAAAAAAAA  
AA

## **FIGURE 18**

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLDSESESEL  
ESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHGEPCHPFLFLDK  
EYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEAARRQMQAEMMYQTGMKIILNGSNKKSQKR  
EAYRYLQKAASMNHTKALERVSYALLFGDYL PQNIQAAREMF EKLTEEGSPKGQTALGFLYASGLGVN  
SSQAKALVYYTFGALGGNLI AHMVLVSRL

**Important features:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 195-199, 217-221, 272-276

**Tyrosine kinase phosphorylation site.**

amino acids 220-228

**N-myristoylation sites.**

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

**Glycosaminoglycan attachment site.**

amino acids 267-271

**Microbodies C-terminal targeting signal.**

amino acids 299-303

**Type II fibronectin collagen-binding domain protein.**

amino acids 127-169

**Fructose-bisphosphate aldolase class-II protein.**

amino acids 101-119

## FIGURE 19

AATTCAGATTTTAAGCCATTCTGCAGTGGAATTTTCATGAACTAGCAAGAGGACACCATCTTCTT  
GTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGAAAAATGCTCTTTTGGGTGCTAGG  
CCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAGACATCACTG  
ATAAGTACATTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCCAGAACCTTTTGAT  
AAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAACAGCTTTAAAGGCAGA  
AACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG  
CCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTGGTGT  
CCCGGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA  
CCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAG  
TTATTAATGTCTCCAGTGTGGAGGTGCCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAA  
TATGCAGTGAAGGTTTCAATGACAGCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTC  
ATGCATTGAACCAGGATTGTTTCAAAACAACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAC  
TCGCCATTTGGGAGCAGCTGTCTCCAGACATCAAACAACAATATGGAGAAGGTTACATTGAAAAA  
AGTCTAGACAAACTGAAAGGCAATAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTG  
CATGGACCACGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAA  
TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAA  
GCAGAGCTGGCTAATCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGA  
AATTGGCCGATTTCAAGAACACATCTCCTTTTCAACCCATTCCTTATCTGCTCCAACCTGGACT  
CATTTAGATCGTGCTTATTTGGATTGCAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGT  
CCCTGCTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCT  
GTATTTAGGCTTTGCCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAATGA  
TCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCAGCATTTACAGTAACTTGTGAATGTTAAGT  
ATCATCTCTTATCTAAATATTAAAAGATAAGTCAACCCAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAA

## **FIGURE 20**

MLFWVLGLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKG FHVIAACLTESG  
STALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDWLTLEDY  
REPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFNDSLRRDMK  
AFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEGYIEKSLDKLKGKNSYVNMD  
LSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQKAELANPKAV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212



## FIGURE 21

CTGAGGCGGCGGTAGCATGGAGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCGGCG  
CACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAAGTAAAA  
GGTGAAGCCAAGAACAGCATTACTGATCCCAAATGGATGATGTTGAAGTTGTTTATACAATTGA  
CATTACAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAGGCGAAGTAAATG  
AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGTTGGTACAAATTCGGT  
CGTCATTACAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACTTGCAGGAGCATTT  
TTCAAACCAAGACCTTGTTTTCTGCTATTAACACCAAGTATAATAACAGAAAGCTGCTCTACTC  
ATCGACTGGAACATTCCCTATATAAACCTCAAAAAGGACTTTTTACAGGGTACCTTTAGTGGTT  
GCCAATCTGGGCATGTCTGAACAACTGGGTTATAAACTGTATCAGGTTCTGTATGTCCACTGG  
TTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTTTGAAGAAGATGGATCCTTAAAGGAGG  
TACATAAGATAAATGAAATGTATGCTTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAAGTG  
GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAAACAGATTAAAACGAGAAATTGA  
GAAAAGGAGAGGAGCACAGATTCAGGCAGCAAGAGAGAAGAACATCCAAAAAGACCCTCAGGAGA  
ACATTTTTCTTTGTCAGGCATTACGGACCTTTTTTCCAAATCTGAATTTCTTCATTATGTGTT  
ATGTCTTTAAAAAATAGACATGTTTCTAAAAGTAGCTGTAACATAACCACCATCTCGATGTAGT  
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCAC  
AAATCATTAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTA  
GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAAT  
GAGCAGCCCAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTC  
CTACATTTGATCCTTTTAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAAC  
ATTTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTTACC  
TGTTTGAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAACATCA  
GATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCATAAGTTGTTGAGGGGAAGGCTTACACAG  
ACACATTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACT  
TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATT  
GAGACCATGTCTATTAAAAAATAAAATGGAAAAGCAAGAATAGCCTTATTTTCAAATATGGAAA  
GAAATTTATATGAAAATTTATCTGAGTCATTAAATTTCTCCTTAAGTGATACTTTTTTAGAAGTA  
CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAAATTTGCAAAACATCATCT  
AAAATTTAAAAA

## **FIGURE 22**

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLGGEVKGEAKNSITDSQMDDVEVVYTIDIQKYI  
PCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQDL  
VFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSSRAV  
QTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA  
QIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSSCNYNHHLDVVDNLTL  
MVEHTDIPEASPASTPQIIKHKALDLDLRWQFKRSRLLDTDQKRSKANTGSSNQDKASKMSSPET  
DEEIEKMKGFGEYSRSPTF

**Important features:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation sites.**

amino acids 75-79, 322-326

**N-myristoylation site.**

amino acids 184-154

**Growth factor and cytokines receptors family.**

amino acids 134-150

## FIGURE 23

GGCACAGCCGCGCGGCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGACGAGCGGACCAGCGCAGGGCAGCCCAA  
 GCAGCGCGCAGCGAACGCCCGCGCCGCCACACCCTCTGCGGTCCCCGCGCGCCTGCCACCCTTCCTCCTTCCCC  
 GCGTCCCCCGCTCGCGGCGCAGTCAGCTTGCCGGTTGCTGCCCGCGGAAACCCGAGGTACACAGCCCGCGCCTCT  
 GCTTCCCTGGGCGCGCGCCCTCCACGCCCTCCTTCTCCCTGGCCCGCGCCTGGCACCGGGGACCGTTGCCTGA  
 CGCGAGGCCAGCTCTACTTTTGGCCCCGCTCTCCTCCGCTGCTCGCCTCTTCCACCAACTCCAACCTCCTTCTCCC  
 TCCAGCTCCACTCGCTAGTCCCGACTCCGCCAGCCCTCGGCCGCTGCCGTAGCGCCGCTTCCCGTCCGGTCCCAAA  
 GGTGGGAACGCGTCCGCCCGCGCCGACCATGCGCACGGTTGCGGTTGCCCGCGCTTCTCTGCACCCTGGCAGTGCTC  
 AGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAGTTGCTCGGAAGTGCGACGTCTTTACGTGTCCAAAGGCTTC  
 AACAGAACGATGCCCCCTCCACGAGATCAACGGTGATCATTGAAGATCTGTCCCAGGGTTCTACCTGCTGCTCT  
 CAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGATGATTCAAAGTGTGGTCAGCGAACAGTGAATCATTG  
 CAAGCTGTCTTTGCTTACGTTACAAGAAGTTGATGAATCTTCAAAGAACTACTTGAAATGCAGAGAAATCCCTG  
 AATGATATGTTTGTGAAGACATATGGCCATTATACATGCAAAATCTGAGCTATTTAAAGATCTCTTCGTAGAGTTG  
 AAACGTTACTACGTGGTGGGAAATGTGAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATG  
 TTCCGCTTGGTGAACCTCCAGTACCACCTTTACAGATGAGTATCTGGAATGTGTAGCAAGTATACGGAGCAGCTGAAG  
 CCCTTCGAGATGTCCCTCGCAAATTGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCGCTACTTTCGCTCAAGGC  
 TTAGCGGTGCGGGAGATGCTGTGAGCAAGGTCTCCGTGGTAAACCCACAGCCAGTGTACCCATGCCCTGTTGAAG  
 ATGATCTACTGCTCCACTGCCGGGCTCTCGTGACTGTGAAGCCATGTTACAACACTGCTCAAACATCATGAGAGGC  
 TGTTTGGCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTA  
 GAGGGTCTTTCAACATTGAATCGGTGATGATCCCATGATGTAAGATTTCTGATGCTATTATGAACATGCAGGAT  
 AATAGTGTCAAGTGTCTCAGAAGGTTTCCAGGGATGTGGACCCCAAGCCCTCCAGCTGGACGAATTTCTCGT  
 TCCATCTCTGAAAGTGCCTTCAGTGCTCGCTTCAGACCACATCACCCGAGGAACGCCCAACACAGCAGCTGGCACT  
 AGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATCTGGTCCCTCCCTGCCAGCAAC  
 GTTTCGAACGATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTAC  
 CTGTTTGCAGTGACAGGAAATGGATTAGCCAACCAGGGCAACAACCCAGAGGTCCAGGTTGACACCAGCAAACAGAC  
 ATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGAATGCATACAATGGGAACGACGTG  
 GACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGAAGTGGCTGTGAGTATCAGCAGTGCCCTTCAGAG  
 TTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGAGAAAGCCGACAGTGTGGTGTCCGTCTGGGGCA  
 CAGGCCTACCTCCTCACTGTCTTCTGCATCTTGTTCCTGGTTATGCAGAGAGTGGAGATAATTCTCAAACCTCTGAG  
 AAAAGTGTTCATCAAAAAGTTAAAGGCACCACTTATCACTTTTCTACCATCCTAGTGACTTTGCTTTTAAATGAA  
 TGGACAACATGTACAGTTTTTACTATGTGGCCACTGGTTAAGAAGTGTGACTTTGTTTTCTCATTAGTTTGGG  
 AGGAAAAGGACTGTGCATTGAGTTGGTTCTGCTCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAA  
 CTATAGTTAGTTGTGCATTTGTGATTTTATCACTCTATTATTGTTTGTATGTTTTTCTCATTTCGTTTGTGGGTT  
 TTTTTTCCAACGTGTATCTCGCCTTGTTCCTACAAGCAAACAGGGTCCCTTCTTGGCACGTAACATGTACGTATT  
 TCTGAAATATTAAATAGCTGTACAGAAGCAGGTTTTATTATCATGTTATCTTATTAAGAAAAAGCCCAAAAGC

## **FIGURE 24**

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQGST  
CCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKS LNDMFVKTYGH  
LYMQNSELFKDLFVELKRYVVG NVNLEEMLNDFWARLLERMFLVNSQYHFTDEYLECVSKYTE  
QLKPFQDVPRKLLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHALLKMIYCSHCRGL  
VTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMAERLEGPFNIESVMDPIDVKISDAIMN  
MQDNSVQVSQKV FQCGPPKPLPAGRISR SISESAFSARFRPHHPEERPTTAAGTSLDRLVTDVK  
EKLKQAKKFWSSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLFAVTGNGLANQGNNPEVQVDT S  
KPDILILRQIMALRVMTSKMK NAYNGNDVDFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAG  
KSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **ATP/GTP-binding site motif A (P-loop).**

amino acids 515-524

#### **N-glycosylation site.**

amino acids 514-518

#### **Glycosaminoglycan attachment sites.**

amino acids 494-498, 498-502

#### **N-myristoylation sites.**

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

#### **Glypicans proteins.**

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

## FIGURE 25

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC  
CTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACT  
TACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAA  
TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCACAGGGACCGAGGC  
CAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAAAGATTGGTTCCTGAG  
AGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCCCTGTGATCATT  
TCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAAACAAGCATTCCAGA  
GCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTG  
AGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTC  
TTCTTCTCCCACCTCACTCTCCCCTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCA  
TGTTTTTCAAGATCATTTTGTGTTGCTCTCTCTAGTGTCTTCTCTCTCGTCAGTCTTAGCCT  
GTGCCCTCCCCCTTACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAACTGTAGCTTCCT  
AGCTAGTGTCAATTAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTT  
AAATGTCAAAAAAAAAAAAAAAAAA

## **FIGURE 26**

MKVLISLLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRRKFM  
TVSGLPKKQCPCDHFKGNVKKTRHQRHHRKPNKHSRACQQLKQCQLRSFALPL

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites.**

amino acids 27-33, 46-52

## FIGURE 27

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAG  
AGCTGGTCTGCCATGGACATCCTGGTCCCCTCCTGCAGCTGCTGGTGCTGCTTCTTACCCTGCC  
CCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCTGTGCAAAGCTACTTCCCCCTACCTGA  
TGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAG  
ATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGGCTGCGGAACCGGAGC  
CAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAAATCCCCACTTTGAGA  
AGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGGCTCCT  
GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGTGTG  
CTCTGTGCAGAGCCCAAGGAAGGTCCTGCAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTGC  
TCTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTT  
GAGCCCACCTGGAACACATTGGGGATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGA  
GAACGCCAGTTCTCCGAAATCCAAATGGAACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTG  
GGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCC  
TTCCCCAGCCTCCAATTAGAACAAAGCCACCCACAGCCTATCTATCTTCCACTGAGAGGGACCTA  
GCAGAATGAGAGAAGACATTGATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC  
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGG  
AAACACTAGGACCTGTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTC  
CCAATGTTGTCCCTTTCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCTGAGGCTACAC  
CCATGCGTCTCTAGGAAGTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGAC  
CCTCTCTCCCCACTACCACCTTCTTCTGAGCTGGGGGACCAGGGAGAATCAGAGATGCTGGGG  
ATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGAA  
ACCACG

## **FIGURE 28**

MDILVPLLQLLVLLLTLPPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRMESKKRELFSSQIKGL  
TGASGKVALLELGCCTGANFQFYPPGCRVTCCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM  
RQLADGSMDDVVCTILVLCVQSPRKVLQEVRRVLRPGGVLFWEHVAEPYGSWAFMWQQVFEPW  
KHIGDGCCLTRETWKDLNAQFSEIQMERQPPPLKWLPGPHIMGKAVKQSFSSKALICSFPSL  
QLEQATHQPIYLPRLGT

**Important features:**

**Signal peptide:**

amino acids 1-23

**Leucine zipper pattern.**

amino acids 10-32

**N-myristoylation sites.**

amino acids 64-70, 78-84, 80-86, 91-97, 201-207



## **FIGURE 29**

CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTACCTATGCTGCTGCTAACGCTGCTGCTGCT  
GCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCCAGAAAGTCTCTCTG  
CCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTCCTGCCTCAT  
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGTGGGGGATGGCTA  
AGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGGCTGCCTTATTTAAA  
GTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTCAATTAAGAAATT  
GTTCCCTTCCCCTGTGTTCAATGTTTGTAAGATTGTTCTGTGTAAATATGTCTTTATAATAAAC  
AGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 30**

MLLLTLLLLLLLLLKGSCLWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQPRG  
EGEKVGDG

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

## FIGURE 31

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAAGTT  
CCTCCAAGCAAGTCATTTCCCTTATTTAACCAGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT  
ATTTGCATCTGTTTTGATAAATGATGTTGACACCTCCACCGAATTCTAAGTGGAATCATGTCGG  
GAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGCTTTGGCCATGATGTTTACC  
TTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTCAATTGGTTATTTTGGGATTGTTGTT  
TGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCAGCATAGAATTGGACA  
CAGAAAGGGAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTATCCACAGGCATCACGGCAGTG  
CTGCTCGTCTTGATTTTTGTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAAATCAC  
AAATAAAGCCATCAGCAGTGCTCCCTTCTGCTGTTCCAGCCACTGTGGACATTGCCATCCTCA  
TTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTGAGCCTGGGAACTGCAGGAGCTGCCAGGTT  
ATGGAAGGCGGCCAAGTGAATATAAGCCCCCTTCGGGCATTCCGTACATGTGGTTCGTACCATTT  
AATTGGCCTCATCTGGACTAGTGAATTCATCCTTGCCTGCCAGCAAATGACTATAGCTGGGGCAG  
TGTTTACTTGTTATTTCAACAGAAGTAAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTC  
TCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAG  
GATTCCGAGAATCATTGTGTCATGTACATGCAAACGCACTGAAAGAACAGCAGCATGGTGCATTGT  
CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTC  
AACCAGAATGCATATACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGC  
ATTCAAATCTTGTTCCAAGAACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAA  
TTTTTCTAGGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACATAC  
AATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGC  
CCATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTTCCTGTGTTTTGCTGTTGATC  
TGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTTCGTA  
AAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGAATGAGGA  
GGGAACAGAATCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCTGGAAAACATT  
TCCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTTT  
TTAAAAGACCTAATAAACCTATTCTTCCTCAAAA

## **FIGURE 32**

MSGRDTILGLCILALALSLAMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYTDNLSIE  
LDTARENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQPLWTFA  
ILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQQMTIA  
GAVVTCYFNRSKNDDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVMYMQLKEQQHG  
ALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD  
FIIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVAHSFLSVFETVLDALFLCFA  
VDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Putative transmembrane domains:**

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

#### **N-glycosylation sites.**

amino acids 204-208, 295-299, 313-317

#### **N-myristoylation sites.**

amino acids 147-153, 178-184, 196-202, 296-275, 342-348

## FIGURE 33

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCCTTAGA  
 ATAATTTGTATGGGATTTGTGATGCAGGAAAGCCTAAGGGAAAAAGAATATTCATTCTGTGTGGT  
 GAAAATTTTTTGAATAAAATTCCTTCTTCAAACAAGGGTGTCTTCTGATATTTATGAGGAC  
 TGTGTCTTCACTATGAAGGCATCTGTTATTGAAATGTTTCTTGTGCTGGTGAAGTGGAGTAC  
 ATTCAAACAAAGAAACGGCAAAGAAGATTAAGGGCCCAAGTTCACTGTGCCTCAGATCAACTGC  
 GATGTCAAAGCCGGAAGATCATCGATCCTGAGTTTATTGTGAAATGTCCAGCAGGATGCCAAGA  
 CCCAAATAGCATGTTTATGGCACTGACGTGTATGCATCCTACTCCAGTGTGTGTGGCGTGCCG  
 TACACAGTGGTGTGCTTGATAATTCAAGAGGGAAAATACTTGTTCGGAAGGTTGCTGGACAGTCT  
 GGTACAAAGGGAGTTATTCCAACGGTGTCCAATCGTTATCCCTACCACGATGGAGAGAATCCTT  
 TATCGTCTTAGAAAGTAAACCCAAAAAGGGTGTAACTACCCATCAGCTCTTACATACTCATCAT  
 CGAAAAGTCCAGCTGCCCAAGCAGGTGAGACCACAAAAGCCTATCAGAGGCCACCTATTCCAGGG  
 ACAACTGCACAGCCGGTCACTCTGATGCAGCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCCAC  
 CACCTTGCCAAAGGCCATCCCCCTTCTGCTGCTTCTACCACAGCATCCCAGACCACAATCAGTGG  
 GCCACAGGAGCCAGGAGATGGATCTTGGTCCACTGCCACCTACACAAGCAGCCAAAACAGAGCCC  
 AGAGCTGATCCAGGTATCCAAAGGCAAGATCCTTCAGGAGCTGCCTTCCAGAAACCTGTTGGAGC  
 GGATGTGAGCCTGGGACTTGTTCAAAAGAAGATTGAGCACACAGTCTTTGGAGCCAGTATCCC  
 TGGGAGATCCAACTGCAAAATTGACTTGTGCTTTTAAATTGATGGGAGCACCAGCATTGGCAAA  
 CGGCGATTCCGAATCCAGAAGCAGCTCCTGGCTGATGTTGCCCAAGCTCTTGACATTGGCCCTGC  
 CGGTCCACTGATGGGTGTTGTCCAGTATGGAGACAACCTTGCTACTCACTTTAACCTCAAGACAC  
 ACACGAATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAAT  
 GTAGGTGCGGCCATCTCCTTTGTGACCAAGAAGTCTTTTCCAAAGCCAATGGAAACAGAGCGG  
 GGCTCCCAATGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT  
 GACTTGGGAGAGAGTCAGGAATCAACATTTTCTTCATCACCATTGAAGGTGCTGCTGAAAATGAG  
 AAGCAGTATGTGGTGGAGCCCACTTTGCAAAACAAGGCCGTGTGCAGAACAAACGGCTTCTACTC  
 GCTCCACGTGCAGAGCTGGTTTGGCCTCCACAAGACCCTGCAGCCTCTGGTGAAGCGGGTCTGCG  
 AACTTGACCGCCTGGCCTGCAGCAAGACCTGCTTGAAGTGGCTGACATTGGCTTCGTATCGAC  
 GGCTCCAGCAGTGTGGGGACGGGCACTTCCGCACCGTCCCTCCAGTTTGTGACCAACCTCACCA  
 AGAGTTTGGAGATTTCCGACACGGACACGCGCATCGGGGCCGTGCAGTACACCTACGAACAGCGGC  
 TGGAGTTTGGGTTCGACAAGTACAGCAGCAAGCCTGACATCCTCAACGCCATCAAGAGGGTGGGC  
 TACTGGAGTGGTGGCACCAGCACGGGGGCTGCCATCAACTTCGCCCTGGAGCAGCTCTTCAAGAA  
 GTCCAAGCCCAACAAGAGGAAGTTAATGATCCTCATCACCAGCGGAGGTCTACGACGACGTCC  
 GGATCCCAGCCATGGCTGCCCATCTGAAGGGAGTGATCACCTATGCGATAGGCGTTGCCTGGGCT  
 GCCAAGAGGAGCTAGAAGTCATTGCCACTCACCCGCCAGAGACCACTCCTTCTTTGTGGACGA  
 GTTTGACAACCTCCATCAGTATGTCCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCAC  
 AGCCTCGGAACGAATTACAGAGCAGGCAGAGCACCAGCAAGTGTGCTTTACTAACTGACGTGTT  
 GGACCACCCACCGCTTAATGGGGCACGCACGGTGCATCAAGTCTTGGCAGGGCATGGAGAAAC  
 AAATGTCTTGTATTATTCTTTGCCATCATGCTTTTTCATATTCCAAACCTGGAGTTACAAAGA  
 TGATCACAAACGTATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACAT  
 TTTGACAATTGTTTTCAAAATAAATGTTCCGAATACAGTGCAGCCCTTACGACAGGCTTACGTAG  
 AGCTTTTGTGAGATTTTAAAGTTGTTATTCTGATTGAACTCTGTAACCCTCAGCAAGTTTCAT  
 TTTTGTGATGACAATGTAGGAATTGCTGAATTAAATGTTTAGAAGGATGAAAAATAAAAAA  
 AA  
 AAG

## **FIGURE 34**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG  
CQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWR  
ESFIVLESKPKKGVTPSALTYSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVA  
TPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQRQDPGAAFOKP  
VGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDI  
GPAGPLMGVVQYGDNPATFNLKTHNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN  
RSGAPNVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAVCRTNG  
FYSLHVQSWFGLHKTLLQPLVKRVCDDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTLQFVTN  
LTKEFEISDTRIGAVQYTYEQRLFQFDKYSSKPDILNAIKRVGYWGGTSTGAAINFALEQL  
FKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIATHPARHDSFF  
VDEFNLHQYVPRIIQNICTEFNSQPRN

### **Important features:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

amino acids 181-200

#### **N-glycosylation sites.**

amino acids 390-394, 520-524

#### **N-myristoylation sites.**

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,  
431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

#### **Amidation site.**

amino acids 304-308

## FIGURE 35

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGC  
CAAACCATGTCTTTTTTCTGTTTTTCAGAGTAGTTCACAACAGATCTGAGTGTTTTAATTAAGCATGGAAT  
ACAGAAAACAACAAAACTTAAGCTTTAATTTTCATCTGGAATTCACAGTTTTCTTAGCTCCCTGGACCC  
GGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTATCACGTGGTGCTCTCCGACTACTCACCCGAGTGTA  
AAGAACCTTCGGCTCGCGTGCTTCTGAGCTGCTGTGGATGGCCTCGGCTCTCTGGACTGTCCCTCCGAGTA  
GGATGTCACTGAGATCCCTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTAC  
CTCAGCCTTCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTTA  
CAGACAAGACTTTCACCTTCACACTTCGAGAGCATTCAAACGTCTCTCATCAAATCCATTTCTGGTCATTC  
TGGTGACCTCCCACCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAGTCT  
TGGTGGGGATATGAGGTTCTTACATTTTCTTATTAGGCCAAGAGGCTGAAAAGGAAGACAAAAATGTTGGC  
ATTGTCTTAGAGGATGAACACCTTCTTTATGGTGACATAATCCGACAAGATTTTTTAGACACATATAATA  
ACCTGACCTTGAAAACCATTATGGCATTCAAGTGCGGTAACTGAGTTTTGCCCAATGCCAAGTACGTAATG  
AAGACAGACACTGATGTTTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGA  
GAAGTTTTTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCCATATTT  
CTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGTATATAATGTCCAGAGAT  
TTGGTGCCAAGGATCTATGAAATGATGGGTCAAGTAAACCCATCAAGTTTGAAGATGTTTATGTCCGGAT  
CTGTTTGAATTTATTAAGGTGAACATTCAATTTCCAGAAGACACAAATCTTTTCTTTCTATATAGAATCC  
ATTTGGATGTCTGTCAACTGAGACGTGTGATTGCAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTT  
TGGCAGGTCACTGCTAAGGAACACCACATGCCATTATTAACCTCACATTCTACAAAAAGCCTAGAAGGACAG  
GATACCTTGTGAAAGTGTTAAATAAAGTAGGTACTGTGAAAATTCATGGGGAGGTCAGTGTGCTGGCTT  
ACACTGAACTGAACTCATGAAAAACCCAGACTGGAGACTGGAGGTTACACTTGTGATTTATTAGTCAGG  
CCCTTCAAAGATGATATGTGGAGGAATTAAATATAAAGGAATTGGAGGTTTTTGCTAAAGAAATTAATAGG  
ACCAACAATTTGGACATGTCAATCTGTAGACTAGAATTTCTTAAAGGGTGTTACTGAGTTATAAGCTCA  
CTAGGCTGTAAAAACAAAACATGTAGAGTTTTATTATTGAACAATGTAGTCACTTGAAGGTTTTGTGTA  
TATCTTATGTGGATTACCAATTTAAAAATATATGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATA  
CTGAACAAAATTTTACCTGTTTTTGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATT  
ATTATTTAAATTAACCTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAGGATAG  
TGAATCATCTTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCACTCCA  
TTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGACCTTGTAAATATTTTACTGTGGT  
AATATAGAGAAGAATTAAAGCAAGAAATCTGAAAA

## **FIGURE 36**

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPITYRQDFHF  
TLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQAEKEDKMLA  
LSLEDEHLLYGDIIRQDFLDTYNNLTTLKTIMAFRWVTEFCPNAKYVMKTDTDVFINTGNLVKYL  
NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQYEPFKVFPPYCSGLGYIMSRDLVPRIYEMMGHV  
KPIKFEDVYVGICLNLKVNIIHIPEDTNLFFLYRIHLDVCQLRRVIAAHGFSSKEIITFWQVMLR  
NTTCHY

Important features:

Type II transmembrane domain:

amino acids 20-39

N-glycosylation sites.

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

Glycosaminoglycan attachment site.

amino acids 239-243

Ly-6 / u-PAR domain proteins.

amino acids 23-37

N-myristoylation site.

amino acids 271-277



## FIGURE 37

CGCTCGGGCACCAGCCGCGGCAAGGATATGGAGCTGGGTTGCTGGACGAGTTGGGGCTCACTTTTCTTCAGCTCCTTCTCATC  
TCGTCTTGCCAAGAGAGTACACAGTCATTAATGAAGCCTGCCCTGGAGCAGAGTGAATATCATGTGTCGGGAGTGCTGTG  
AATATGATCAGATTGAGTGCCTGCCCCGAAAGAGGGAAGCTGGGTTATACCATCCCTTGCTGCAGGAATGAGGAGAA  
TGAGTGTGACTCCTGCCTGATCCACCAGGTTGTACCATCTTTGAAAACGCAAGAGCTGCCGAAATGGCTCATGGGGGGGT  
ACCTTGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAGTGCCGAGCAGGCTGGTACGGAGGAGACTGCATGCGATGTG  
GCCAGGTTCTGCGAGCCCCAAAGGGTCAGATTTTGTGGAAAGCTATCCCTTAAATGCTCACTGTGAATGGACCATTTCATGC  
TAAACCTGGGTTTGTATCCAACTAAGATTTGTGATGTTGAGTCTGGAGTTTGACTACATGTGCCAGTATGACTATGTTGAG  
GTTTCGTGATGGAGACAACCGCATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAG  
GATCCTCACTCCACGTCTCTTCCACTCCGATGGCTCCAAGAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGC  
ATGCTCCTCATCCCTTGTTTCCATGACGGCACGTGCGTCTTGACAAGGCTGGATCTTACAAGTGTGCTGCTTGGCAGGC  
TATACTGGGCAGCGCTGTGAAAATCTCCTTGAAGAAAGAACTGCTCAGACCCGCGGGGCCAGTCAATGGGTACCAGAAAA  
TAACAGGGGGCCCTGGGCTTATCAACGGACGCCATGCTAAAATTTGGCACCGTGGTGTCTTTCTTTTGAACACTCCTATGT  
TCTTAGTGGCAATGAGAAAAGAACTTGCCAGCAGAAATGGAGAGTGGTCAGGGAAACAGCCCATCTGCATAAAAGCCTCCCGA  
GAACCAAAGATTTAGACCTGGTGAGAAGGAGAGTTCTTCGATGCAGGTTCAAGGAGACACCATTACACCAGCTAT  
ACTCAGCGGCCCTTCAAGCAGAGAACTGCAGAGTGCCCTTACCAAGAAGCCAGCCCTTCCCTTTGGAGATCTGCCCATGGG  
ATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACCTTCTACCGCCGCTGGGCAGCAGCAGGAGGACATGT  
CTGAGGACTGGGAAGTGGAGTGGGCGGGCACCATCCTGCATCCCTATCTGCGGGGAAATGAGAACATCACTGCTCCAAAGA  
CCCAGGGTTGCGCTGGCCGTGGCAGGCAGCCATCTACAGGAGGACCAGCGGGGTGCATGACGGCAGCTTACACAAGGGAGC  
GTGGTTCTTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCACTGTGTTACTGACCTGGGGAAG  
GTCACCATGATCAAGACAGCAGACCTGAAAGTTGTTTTGGGGAAATTTACCGGGATGATGACCGGGATGAGAAGACCATCC  
AGAGCCTACAGATTTCTGCTATCATTTGCTATCCCAACTATGACCCCATCCTGCTTGATGCTGACATCGCCATCCTGAAGCT  
CCTAGACAAGGCCGTATCAGCACCAGGAGTCCAGCCCATCTGCTCGCTGCCAGTCCGGATCTCAGCACTTCCCTCCAGGAG  
TCCCACATCACTGTGGCTGGCTGGAATGTCTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGG  
TGGTCAGTGTGGTGGATCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGAGTGTCACTGATAACATGTT  
CTGTGCCAGCTGGGAACCCACTGCCCCCTTCTGATATCTGCACTGCAGAGACAGGAGGCATCGCGGCTGTGCTTCCCGGGA  
CGAGCATCTCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCA  
CTGCTTTCACCAAGGTGCTGCTCTTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAG  
TGTTTCTGTATATCCGTCTGTACGTGTGTCATTGCGTGAAGCAGTGTGGGCTGAAGTGTGATTGCGCTGTGAACTTGGCT  
GTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAAGTACCTCCATTGCTGGTAGGCTGATGCCGCTCCA  
CTACTAGGACAGCCAATTGGAAGATGCCAGGGCTTGCAAGAAGTAAGTTCTTCAAAGAAGACCATATACAAAACCTCTCCA  
CTCCACTGACCTGGTGGTCTTCCCCAACTTTTCAGTTATACGAATGCCATCAGCTTGACCAGGGAGATCTGGGCTTCATGAG  
GCCCCTTTTGAGGCTCTCAAGTTCTAGAGAGCTGCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGCATGCTT  
TGTGTACATGGCCACAGTACAGTCTGGTCTTTTCCCTTCCCATCTCTTGTACACATTTTAAATAAAATAAGGGTTGGCTTCT  
GAACTACAAAAA  
AAAAA

## **FIGURE 38**

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYT  
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGDCMRCGQ  
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDQII  
KRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC  
ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNNSYVLSGNE  
KRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPQVQSRETPLHQLYSAAFQKQKLSAPTK  
KPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGIENITAP  
KTQGLRWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVAAHCVDLGLKVTMIKTADL  
KVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASR  
DLSTSFAQESHITVAGWNVLADVRSPGFKNDTLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCA  
SWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMLVSWSYDKTCSHRLSTAFTKVLPFKDWI  
ERNMK

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-23

#### **EGF-like domain cysteine pattern signature.**

amino acids 260-272

#### **N-glycosylation sites.**

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

#### **N-myristoylation sites.**

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,  
474-480, 491-497, 638-644, 666-672

#### **Amidation site.**

amino acids 56-60

#### **Serine proteases, trypsin family.**

amino acids 489-506

#### **CUB domain proteins profile.**

amino acids 150-167

## FIGURE 39

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCGTGATTTATTAACGTGGCTTAATC  
TGAAGGTTCTCAGTCAAATCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGCTTGGCTGG  
TTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAAATGAAGGCGCTTCTGTTGC  
TGGTCTTGCCCTTGGCTCAGTCTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCCTGTATTTCAGAACTCTGTA  
AAGGTGCCTCCCACTACGGCCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAGACGGCTGTGCGAGCC  
TCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAATGACAGACGAGCCTGGCCTAGACA  
ACCTTGCTACGTGTCTCGGAGAGGACGGGCAGCCAGCAATCAGCCAGTGGACTCTGGCCGGAGCAACCGAATA  
GGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTAAAAAATAAATCGAGCTTTGAGTGTTCTTCGAA  
GGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACCAGGGCAGGGAAAATTCTGAAAACACCACTGCCCTGAAG  
TCTTTCCAAGGTTGTACCACCTGATCCAGATGGTGAATTAACAGCATCAAGATCAATCGAGTAGATCCAGTGAAA  
GCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCCACTGGTCCATATCATTATCCAACACATTATCGTGATGGGG  
TGATGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTC  
ACAACTACGCTGTGCGTCTCCTGCGGAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAAGTCCGCA  
GCAGGAACAATGGACAGGCCCGGATGCCTACAGACCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCC  
CCGAGGAGCAGCTTGAATAAACTGGTGCGCAAGGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGCTGGATGGCG  
GTGTGGCATATCGACATGGTCAGCTTGAGGAGAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCA  
GCCAGAAAAGTGGGCTCATCTGATTAGGCCAGTGAAGACGTGTTACCTCGTGTGTCGCCGAGGTTCCGGCAGC  
GGAGCCCTGACATCTTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCAGGGCCAGGGAGAGGAGCAACA  
CTCCCAAGCCCTCCATCTACATACTTGTGTCATGAGAAGGTGTAATATCCAAAAGACCCCGGTGAATCTCTCG  
GCATGACCGTCGCAGGGGAGCATCACATAGAGAATGGGATTGCTATCTATGTCATCAGTGTGAGCCCGAGGAG  
TCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTTTGTGAATGTGGATGGGGTCGAACTGACAGAGGTCAGCC  
GGAGTGAGGCACTGGCATTATTGAAAAGAACATCATCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGC  
CCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGACTGGTCCCCATCCT  
GGGTGATGTGGCTGGAATTACCACGGTGCTTGTATAACTGTAAAGATATTGTATTACGAAGAAACACAGCTGGAAGTC  
TGGGCTTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAAACAAACCTTTTTTCATCAATCCATTGTTGAAGGAA  
CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTGCTGTCAATGGTAGAAGTACATCAGGAATGA  
TACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAACTATTGTTTCTTGGCCTGGCACTT  
TTTTATAGAATCAATGATGGGTGAGGAGAAACAGAAAAATCACAAATAGGCTAAGAAGTTGAAACACTATATTTATC  
TTGTCAGTTTTATATTTAAAGAAGAATACATTGTAAAAATGTCAGGAAAAGTATGATCATCTAATGAAAGCCAGTT  
ACACCTCAGAAAATATGATTCCAAAAAATTAACCTACTAGTTTTTTTTCAGTGTGGAGGATTTCTCATTACTCTAC  
AACATTGTTTATATTTTCTATTCAATAAAAGCCCTAAACAACATAAATGATTGATTGTATACCCCACTGAATT  
CAAGCTGATTTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGGTACATTATGGCCATTTTAAATTTACAGCT  
AAAAATTTTTTAAATGCATTGCTGAGAAACGTTGCTTTCATCAACAAGAATAAATATTTTTTCAGAAGTTAAA

## **FIGURE 40**

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCASLTATAPS  
PEVSAAATISLMTDEPLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRSEFKKINR  
ALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVDPSELSIRLV  
GGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVM  
REQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVKRVDEPGVFIFNVLDGGVAYRHG  
QLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVRSPDIFQEAGWNSNGSWSPG  
PGRSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHREWDLPIYVISVEPGGVISRDGR  
IKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPP  
SDWSPSWVMWLELPRCLYNCKDIVLRNTAGSLGFCIVGGYEEYNGNKPFPIKSIVEGTPAYNDG  
RIRCGDILLAVNGRSTSGMIHACLARLLKELKGRITLTIVSWPGTFL

**Important features:**

**Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-112, 157-161, 289-293, 384-388

**Tyrosine kinase phosphorylation sites.**

amino acids 433-441, 492-500

**N-myristoylation sites.**

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,  
467-473, 603-609

## FIGURE 41

ACCAGGCATTGTATCTTCAGTTGTCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTT  
CTTGCCCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGCTTCAACCTGACT  
TTCCACCTTTTCCTACAAATTCGATTACTGTTGCTGTTGACTTTTGTGCTGACAGTGGTTGGGTGGGC  
CACCAGTAACTACTTCGTGGGTGCCATTCAAGAGATTCTTAAAGCAAAGGAGTTCATGGCTAATTTCC  
ATAAGACCCCTCATTTTGGGGAAGGGAAAACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAATT  
GACAACTGTCTTCTGTGTCTCCTTACCTCAGAGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCAC  
TTTGGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAG  
CTTTACAGAGGGTGCCTCCTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAA  
CATCTGCATCCCTTCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGG  
TAAAAAGTTTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGG  
ACTGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAG  
CATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTTGG  
GGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACTACTGCGGAT  
GGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGGCCCTG  
CCTGAAGTGGGTAAATATACAATGGTCTTCCACTAGAGACAAAGCAATGAGGTGAACGCAGAACG  
GATGAAGCTCTTACACCAAGTGTACGAGTCTGGAGAACAGATGGGTTGAGTAGTTGTTCTTATAAAT  
TAGTATCTGTGGAACACAATCCTTTATATATCAACATCACAGTGGATTCTGGTTTGGTGCATGACCC  
TGGATCTTTTGGTGATGTTTGAAGAACTGATTCTTTGTTTGAATAATTTTGGCCTAGAGACTTCAA  
ATAGTAGCACACATTAAGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTCTTTTGTATTTTCT  
TAGCAGAGCTCCTGGTGATGTAGAGTATAAACAGTTGTAACAAGACAGCTTTCTTAGTCATTTTGAT  
CATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGATAA  
AATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATATTATGGGAT  
AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAA  
AGGTACGAAGATACAATACTGTTATTCAATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGTGAGGT  
GAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAAGTGGGAATGAAGA  
GGTAGCAGGAGGGTGGAGTGTGCGCTGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC  
CTTCAGGGGAGGACCTGCCAGGTATGCCTTCCAGTGATGCCACCAGAGAATACATTCTCTATTAGT  
TTTTAAAGAGTTTTTGTAAATGATTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACAT  
ATTAATAATAATAATATGTCTATCAAATACCTCTGTAGTAAAATGTGAAAAAGCAAAA

## **FIGURE 42**

MGFNLTFFHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLILGKGKTLTN  
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPH  
RNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEENWDCFIHFDV  
DLVPENDFNLYKCEEHPKHLVGRNSTGYRLRYSGYFGGVTALSREQFFKVNGFSNNYWGWWGED  
DDLRLRVELQRMKISRPLPEVGKYTEMFHTRDKGNEVNAERMKLLHQVSRVWRTDGLSSCSYKLV  
SVEHNPLYINITVDFWFGA

**Important features:**

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 4-8, 220-224, 335-339

**Xylose isomerase proteins.**

amino acids 191-202

### **FIGURE 43**

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCTGGG  
CCGCTTGCCCTCCTGCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCACAACAG  
ACGGGACAACCTTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTGGATGCCCAT  
GTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCTGCGGCTGCTGTC  
ATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTGCCCCGTCCCCCTCCC  
TTCCTTATTTATTCTGCTGCCCCAGAACATAGGTCTTGGAATAAAATGGCTGGTTCTTTGTTT  
TCCAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 44**

MALSSQIWAACLLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPI  
CIFCCGCCHRSKCGMCCKT

**Important features:**

**Signal peptide:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 58-59

**N-myristoylation site.**

amino acids 44-50

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 1-12



## FIGURE 45

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCC  
TCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT  
TCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTG  
GACCTTCAACACAACCCCTCTTGTCAACATACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA  
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAG  
AAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCA  
GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCA  
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATT  
TATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTC  
CTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCGTGCAGCAGAACT  
TCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCCATG  
GTCCTCCTGTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTG  
GTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGGG  
AAACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT  
AGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAAAGAT  
GGAAAATCCCCACTCACTGCTCAGGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTA  
TCTAGACAGCAGTGCACTCCCCTAAGTCTCTGCTCA

## **FIGURE 46**

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQP  
EGGTIIIVTQNRNRERVDFFDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLK  
PKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFIC  
VARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE  
EKRRVDICRETPNICPHSGENTHEYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDT  
PRLFAYENVI

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **Transmembrane domain:**

amino acids 224-250

#### **Leucine zipper pattern.**

amino acids 229-251

#### **N-glycosylation sites.**

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,  
291-295

## FIGURE 47

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGG  
ATTTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCT  
TAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTCCCAGGAATT  
ATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTG  
CTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCACAGTCATTGGTGCTC  
TGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTCATGTGTAATTCTCCAAGC  
AACAGTAATGCCAATTGTGAATTTTCATTGAAAACATCAGTGACATTTCATCCAGAATCCTTCAA  
CTTGCAAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTCAATAAACCCACCAGTAACG  
ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGG  
CTTATCCACTTCTCAGTATTTTTAGGTCTATTGCTTGTGGAATTCTGGAGGTCCTGTTTGGGCT  
CAGTCAGATAGTCATCGGTTTCTTGGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTG  
TGTAGTTTAAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAAAAAA

## **FIGURE 48**

MTCEGWTSCNGFSLVLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA  
TTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCM LISIQALLKGPLMCNSPSNSNANCEFSL  
KNISDIHPESFNLQWFFENDSCAPPTGFNKPTSNDTMASGWRASSFHF DSEENKHLIHF SVFLGL  
LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

### **Important features:**

#### **Transmembrane domains:**

amino acids 10-31 (type II), 50-72, 87-110, 191-213

#### **N-glycosylation sites.**

amino acids 80-84, 132-136, 148-152, 163-167

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 223-227

#### **N-myristoylation sites.**

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 207-218

#### **TNFR/NGFR family cysteine-rich region protein.**

amino acids 4-12

## **FIGURE 49**

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGA  
AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG  
ATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTCGAACTGTGA  
CATGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGAAGCCAATGACC  
CATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC  
TGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAAATGCAAATACAAGAG  
CAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTCTGCCA  
CTACTTGCTTCAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACC  
TCCTCCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCCCT  
TTCTGATCAGGAGGCTTCTTTATGAATTAACTCGCCCCACCACCCCTCA

## **FIGURE 50**

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKS  
SQKQHSPVPEKAIPILITPGSATTC

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 36-59

N-myristoylation sites.

amino acids 41-47, 45-51, 84-90

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.

amino acids 54-67

## FIGURE 51

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGG  
AGGACAGGGAGTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCGGCAAGG  
AGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATGAAGTTCCAG  
GGGCCCTTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGGCCCCCTGCAGAG  
CGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGACATGGCCTGGGAGACGCCCTGA  
GCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGAGGGGCAGCTGGCTCTAAAGTCAGTGAG  
GCCCTTGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAGGCAGGTTCCAGGCTTTGGCGC  
AGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATGCTCTGGGAAACACTGGGCACGAGA  
TTGGCAGACAGGCAGAAGATGTCATTGACACGGAGCAGATGCTGTCCGCGGCTCCTGGCAGGGG  
GTGCCTGGCCACAGTGGTGTCTGGGAACTTCTGGAGGCCATGGCATCTTTGGCTCTCAAGGTGG  
CCTTGGAGGCCAGGGCCAGGGCAATCCTGGAGGTCTGGGGACTCCGTGGGTCCACGGATACCCCG  
GAAACTCAGCAGGCAGCTTTGGAATGAATCCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGA  
GGGCCACCAAACCTTTGGGACCAACACTCAGGGAGCTGTGGCCCAGCCTGGCTATGGTTCAGTGAG  
AGCCAGCAACCAGAATGAAGGGTGACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCA  
ACTCTGGGGGAGGCAGCGGCTCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAAC  
AATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAG  
TGGCGGCAGCAGTGGTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGT  
CCTCCTGGGGATCCAGCACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGCGGAGGAAATGGA  
CATAAACC CGGTGTGAAAAGCCAGGGAATGAAGCCCGGGGAGCGGGGAATCTGGGATT CAGGG  
CTTCAGAGGACAGGGAGTTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATCGCCTCCTTG  
GAGGCTCTGGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGTT  
GGTGGAGTCAATACTGTGAACCTCTGAGACGTCTCCTGGGATGTTTAACTTTGACACTTTCTGGAA  
GAATTTTAAATCCAAGCTGGGTTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGAAGCTCTC  
GCATCCCGTGACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCCACTCCCTCCTTAA  
AACACCACCCTCTCATCACTAATCTCAGCCCTTGCCCTTGAAATAAACCTTAGCTGCCCCACAAA  
AA  
AA

[illegible]

Signal peptide:

N-glycosylation site.

Glycosaminoglycan attachment site.

Casein kinase II phosphorylation site.

N-myristoylation site.

Cell attachment sequence.

APP ID=10063534



## FIGURE 53

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGG  
CTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCT  
ACTCGCCCGCATCCTGGCTTGACCTATGCCTTCTATAACAACCTGCCGCCGGCTCCAGTGTTTCC  
CACAGCCCCCAAACGGAACGGTTTTTGGGGTCACCTGGGCCTGATCACTCCTACAGAGGAGGGC  
TTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCCAGGGCTTTACGGTATGGCTGGGTCCCAT  
CATCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCACCAATGCCTCAGCTGCCA  
TTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGGCTGGGAGAAGGGATACTGCTG  
AGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCGCCTTCCATTTCAACATCCT  
GAAGTCTATATAACGATCTTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGG  
CCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGGAGCACATCAGCCTCATGACCTTGGACAGTCTA  
CAGAAATGCATCTTCAGCTTTGACAGCCATTGTGAGGAGAGGCCAGTGAATATATTGCCACCAT  
CTTGAGACTCAGTGCCCTTGTAGAGAAAAGAAGCCAGCATATCCTCCAGCACATGGACTTTCTGT  
ATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCCTGGTGATGACTTCACAGAC  
GCTGTATCCGGGAGCGCGCTCGCACCCCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAA  
AGCCAAGTCCAAGACTTTGGATTTTATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG  
CATTGTGAGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACG  
GCCAGTGGCCTCTCCTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCG  
ACAGGAGGTGCAAGAGCTTCTGAAGGACCGGATCCTAAAGAGATTGAATGGGACGACCTGGCCC  
AGCTGCCCTTCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATC  
TCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTG  
CCTCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATCCTGAGGTCTACGACC  
CCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCTCTTCTCCGCA  
GGGCCCAGGAAGTGCATCGGGCAGGCGTTGCCATGGCGGAGATGAAAGTGGTCCTGGCGTTGAT  
GCTGCTGCACTTCCGGTTCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAATTGATCATGC  
GCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGCACTGACTTTCTGAC  
CCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGCTGTCAA

## **FIGURE 54**

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPPKRNWFWGHLG  
LITPTEEGLKDSTQMSATYSQGFTVWLGPPIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP  
WLGEIGILLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI  
SLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHDGRRFHRAC  
RLVHDFTDVIRERRRTLPTQGIDDFKDKAKSKTLDLDFIDVLLLSKDEDGKALSDEDIRAEADTF  
MFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR  
LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENSKGRSP  
LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN  
VGLQ

### **Important features:**

#### **Transmembrane domains:**

amino acids 13-32 (type II), 77-102

#### **Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 461-471

#### **N-glycosylation sites.**

amino acids 112-116, 168-172

## **FIGURE 55**

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTTGA  
GCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTTCTGCCT  
TTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCATTGACGTGG  
TACAGCCTTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTGTTTGGCGTGTGCTTGC  
ATAATTTCATGGCCAGTTTATGAAGCTTTGGAAGGCACTATGGACAGAAGCTGGTGGACAGTTTT  
GTAACATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCTTGACGAATGTGTTGCTT  
GTGATTCGAACATTTGAGGGTTACTTTTGAAGCAACAATACATTCTCGAACCTGAATGTCAGTA  
GCACAGGATGAGAAGTGGGTCTGTATCTTGTGGAGTGGAATCTTCCTCATGTACCTGTTTCCTC  
TCTGGATGTTGTCCCACTGAATTCCCATGAATACAAACCTATTTCAGCAACAGCAAAAAAAAAA  
AAA

## **FIGURE 56**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGALIFCILQSLALTWYSLSFIPFAR  
DAVKKCFVCLA

Important features:

Signal peptide:

amino acids 1-33

Type II fibronectin collagen-binding domain protein.

amino acids 30-72

## FIGURE 57

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGAGTGGAGCAGCCAGCAGGCCGCCAACATGCTCTGTCTGTGCCTG  
TACGTGCCGGTTCATCGGGGAAGCCAGACCGAGTTCAGTACTTTGAGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCC  
ATTTTCAAGCTCAGTGTCTTCATCCCTCCAGGAATTCACACCTACCGCCAGTGGAGCAGAAAAATGTACAAGCT  
GGAGATAAGGACCTTGATGGGCAGCTAGACTTTGAAGAATTTGTCCATTATCTCCAAGATCATGAGAAGAAGCTGAGG  
CTGGTGTTTAAGATTTTGGACAAAAAAGATGATGGACGCATTGACGCGCAGGAGATCATGCAGTCCCTCGGGGACTTG  
GGAGTCAAGATATCTGAACAGCAGGCAGAAAAAATTCACAGAGCATGGATAAAACGGCAGCATGACCATCGACTGG  
AACGAGTGGAGAGACTACCACCTCCTCCACCCCGTGGAAAAACATCCCGAGATCATCCTCTACTGGAAGCATTCCACG  
ATCTTTGATGTGGGTGAGAATCTAACGGTCCCGGATGAGTTCACAGTGGAGGAGAGGCAGACGGGGATGTGGTGGAGA  
CACCTGGTGGCAGGAGGTGGGGCAGGGGCCGTATCCAGAACCTGCACGGCCCCCTGGACAGGCTCAAGGTGCTCATG  
CAGGTCCATGCCTCCCGCAGCAACAACATGGGCATCGTTGGTGGCTTCACTCAGATGATTGAGAAGGAGGGGCCAGG  
TCACTCTGGCGGGCAATGGCATCAACGTCTCAAAATTGCCCGGAATCAGCCATCAAATTCATGGCCATGAGCAG  
ATCAAGCGCCTTGTGGTAGTGACAGGAGACTCTGAGGATTACAGAGAGGCTTGTGGCAGGCTCCTTGGCAGGGGCC  
ATCGCCAGAGCAGCATCTACCCAATGGAGTCTGAAGACCCGGATGGCGCTCGCGAAGACAGGCCAGTACTCAGGA  
ATGCTGGACTGCGCCAGGAGGATCCTGGCCAGAGAGGGGTGGCCGCTTCTACAAAGGCTATGTCCCAACATGCTG  
GGCATCATCCCTATGCCGCGCATGCACCTTGAGTCTACGAGACGCTCAAGAAATGCCTGGCTGCAGCACTATGCAGTG  
AACAGCGGGGACCCCGGCTGTGTGTCTCCTGGCCTGTGGCACCATGTCCAGTACCTGTGGCCAGCTGGCCAGCTAC  
CCCCTGGCCCTAGTCAGGACCCGGATGCAGGCGCAAGCCTCTATTGAGGGCGCTCCGGAGGTGACCATGAGCAGCCTC  
TTCAAACATATCCTGCGGACCGAGGGGCCCTTCGGGCTGTACAGGGGGCTGGCCCCAACTTCATGAAGGTCACTCCA  
GCTGTGAGCATCAGCTACGTGGTCTAGGAGAACCTGAAGATCACCTGGGCGTGCAGTCGCGGTGACGGGGGAGGGC  
CGCCCGCAGTGGACTCGCTGATCCTGGGCGCAGCCTGGGGTGTGCAGCCATCTCATTCTGTGAATGTGCCAACACT  
AAGCTGTCTCGAGCCAAGCTGTGAAAACCTAGACGCAACCCGACGGGAGGGTGGGGAGAGCTGGCAGGCCAGGGCTT  
GTCCTGCTGACCCAGCAGACCCTCCTGTTGGTTCCAGCGAAGACCACAGGCATTCTTAGGGTCCAGGGTGCAGCAGG  
CTCCGGGCTCACATGTGTAAAGACAGGACATTTCTGCACTGCCTGCCAATAGTGAGCTTGAGCCTGGAGGCCGGCT  
TAGTTCCTCCATTTACCCCTTGACCCAGCTGTTGGCCACGGCCCTGCCCTCTGGTCTGCCGTGCATCTCCTGTGC  
CCTCTGCTGCCTGCCTGTCTGCTGAGGTAAGGTGGGAGGAGGGCTACAGCCACATCCACCCCTCGTCCAATCCC  
ATAATCCATGATGAAGGTGAGGTACGCTGGCCTCCAGGCCCTGACTTCCCAACCTACAGCATTGACGCCAATCTGGC  
TGTGAAGGAAGAGGAAGGATCTGGCCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATG  
CTTGGGAGTGCAGGGGGCTCGGGCTGCCTGGCCTGGCTGCACAGAAGGCAAGTGTGGGGCTCATGGTGTCTGAGCT  
GGCTGGACCTGTGAGGATGGGCCCCACCTCAGAACCAACTCACTGTCCCCACTGTGGCATGAGGGCAGTGGAGCA  
CCATGTTTGGAGGGCAAGGGCAGAGCGTTTGTGTCTCTGGGAGGGAAGGAAAGGTGTTGGAGGCCCTAATTATGG  
ACTGTTGGGAAAAGGTTTGTTCAGAAAGGACAAGCCGACAAATGAGCGACTTCTGTGCTTCCAGAGGAAGACGAGG  
GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGTTCCTGTCCAACCCAGCAGGGGCGCAGC  
GGGACAGCCCCACATTCACCTGTGTCACTGCTTGGAACTTATTTATTTGTATTTATTTGAACAGAGTTATGTCCT  
AATATTTTATAGATTTGTTAATTAATAGCTTGTCACTTTCAAGTTCATTTTATTCATATTTATGTTTATGTT  
GATGTACCTTCCCAAGCCCGCCAGTGGGATGGGAGGAGGAGGAGAGGGGGGCTTGGGCCGCTGCATGCATCATCT  
GTCCAGAGAAATTCCTTTTGGGACTGGAGGAGAGAAAGCGGCCAGAGGAGCAGCCCTGGCTCCTTTCTTTGGCAG  
GTTGGGGAAGGGCTTGCCCCAGCCTTAGGATTTAGGGTTTGAAGTGGGGGCTGGAGAGAGAGGGAGGAACCTCAAT  
AACCTTGAAGGTGGAATCCAGTTATTTCTGCGCTGCGAGGGTTTCTTTATTTCACTCTTTTCTGAATGTCAAGGCAG  
TGAGGTGCCTCTCACTGTGAATTTGTGGTGGCGGGGGCTGGAGGAGAGGGTGGGGGCTGGCTCCCTCCCTCCAGC  
CTTCTGCTGCCCTTGTCTAACAATGCCGGCCAATGGCGACCTCACGGTTGCACTTCCATTCACAGAAATGACCTGA  
TGAGGAAATCTTCAATAGGATGCAAGATCAATGCAAAATTTGTTATATATGAACATATAACTGGAGTGTGCAAAAG  
CAAATTAAGAAAGAAATGGACGTAGAGTTGTCAATTTAAAGCAGCCTTCTAATAAAGTTGTTTCAAAGCTGAAAAAA  
AA

## **FIGURE 58**

MLCLCLYVPVIGEAEQTEFYFESKGLPAELKSI FKL SVFIP SQEFSTYRQWKQKIVQAGDKDL DG  
QLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQA EKILKSMDKNG  
TMTIDWNEW RDYHLLHPVENIPEI ILYWKHSTIFDVGENLTPDEFTVEERQTGMWWRHLVAGGG  
AGAVSRTCTAPLDR LKVL MQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESA IK  
FMAYEQIKRLVGSDQETLRIHERLVAGSLAG AIAQSSIYPMEVLKTRMALRKTGQYSGMLDCARR  
ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKN AWLQHYAVNSADPGVFVLLACGTMSSTC  
GQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGA FGLYRGLAPNFMKVIPAVSISYV  
VYENLKITLGVQSR

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Putative transmembrane domains:**

amino acids 284-304, 339-360, 376-394

#### **Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

#### **N-glycosylation sites.**

amino acids 129-133, 169-173

#### **Elongation Factor-hand calcium-binding protein.**

amino acids 54-73, 85-104, 121-140

## FIGURE 59

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGC  
TTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG  
CACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTGCGCTCAGCT  
GGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAAACCTTCTGATAT  
CGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCAAAGATG  
AGCTGTGCGAGCAGGATGAAATGTTTTCAGAGGCCGGACAGCAGTGTGCTGATCAAGTGATAGTT  
GGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT  
CATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGG  
AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCC  
CAGCCCACAGTGGTCTGGGCATCCCCAGTTGACCAGGGAGCCAACTTCTCGGAAGTCTCCAATAC  
CAGCTTTGAGCTGAACTCTGAGAATGTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGA  
TCAACAACACATACTCCTGTATGATTGAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTG  
ACAGAATCGGAGATCAAAGGCGGAGTCACCTACAGCTGCTAACTCAAAGGCTTCTCTGTGTGT  
CTCTTCTTTCTTTGCCATCAGCTGGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAAAT  
GTGCCTTGCCACAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTTAC  
CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG  
AGCAAACAAGAGCAAGAAACAAAAAGCAAGCAAGGCTCCAATATGAACAAGATAAAT  
CTATCTTCAAAGACATATTAGAAGTTGGGAAATAATTCATGTGAAGTAGACAAGTGTGTTAAGA  
GTGATAAGTAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT  
CACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGC  
TGTAATGTTGCTCTGAGGAAGCCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATCCAC  
AAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCG  
GCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTATGATGCTTCCAAAGGTGCCTTGGCTTC  
TCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGT  
CGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 6o**

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS  
DIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKKNVQLTDAGTYKC  
YIITSKKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFQPTVVWASQVDQGANFSEVS  
NTSFELNSENVTMKVVSVLNVNTINNTYSCMIENDIAKATGDIKVTESI KRRSHLQLLNSKASL  
CVSSFFAISWALLPLSPYIMLK

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 258-281

#### **N-glycosylation sites.**

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,  
220-224

#### **N-myristoylation sites.**

amino acids 52-58, 126-132, 188-194



## FIGURE 61

TGACGTCAGAATCACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAG  
CACCAGGAGCCCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGT  
GGGCTACCCCCTGGTGGTGGTTATGGGGTCTGCCCCCTGGAGGGCCTTATGGACCACCAGCTGG  
TGGAGGGCCCTATGGACACCCCCAATCCTGGGATGTTCCCCCTCTGGAACCTCAGGAGGACCATATG  
GCGGTGCAGCTCCCGGGGGCCCCCTATGGTCAGCCACCTCCAAGTTCCTACGGTGCCAGCAGCCT  
GGGCTTTATGGACAGGGTGGCGCCCCCTCCCAATGTGGATCCTGAGGCCTACTCCTGGTTCCAGTC  
GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA  
ATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCA  
GGCCGCATCGATGTCTACGGCTTCTCAGCCCTGTGGAATTCATCCAGCAGTGAAGAACCCTCTT  
CCAGCAGTATGACCGGGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCC  
AAATGGGCTACAACCTGAGCCCCCAGTTCACCCAGCTTCTGGTCTCCCGCTACTGCCACGCTCT  
GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCCACCGCTGCAGGTGCTGACAGA  
GGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCTCAGCTTCGAGGACTTCGTCA  
CCATGACAGCTTCTCGGATGCTATGACCCCAACCATCTGTGGAGAGTGGAGTGCACCAGGGACCTT  
TCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTTCTGTCCCTCTAGAAGAAC  
ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCTGTCATCATAGCCACCA  
AATAGTGAGGACCGGGCTGAGGCCACACAGATAGGGGCTGATGGAGGAGAGGATAGAAGTTGA  
ATGTCCTGATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCCCTTGTAATGG  
AGTTAGTGTCCAGTCAGCTGAGCTCCACCCTGATGCCAGTGGTGAGTGTTCATCGGCCTGTTACC  
GTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAACGAGCCCATTTTCTCCAAAGTGAAT  
CTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGGATTCTGCCACACCCATAAAT  
CCTTGTTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGGCAT  
CTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCCCTGCCATGCTCTGCTCGGCT  
TCAGTCTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTAATTGCAATTTTTTTTC  
ATTTGGGGCCAAAAGTCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

## **FIGURE 62**

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG  
HPNPGMFPSGTPGGPYGGAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVSDH  
SGYISMKELKQALVNCNWSSFNDETCMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDR  
DRSGSISYTELQQALSQMGYNLSPQFTQLLVSRYPFRSANPAMQLDRFIQVCTQLQVLTEAFREK  
DTAVQGNIRLSFEDFVTMTASRML

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 147-150

**Casein kinase II phosphorylation sites.**

amino acids 135-138, 150-153, 202-205, 271-274

**N-myristoylation sites.**

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-66, 70-75, 78-83, 83-88, 87-92, 110-115

## FIGURE 63

CAGGATGCAGGGCCGCGTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCCTGGTCTGTCTTCATC  
TCCCAGGCCTCTTTGCCCCGAGCATCGGTGTTGTGGAGGAGAAAGTTTCCCAAACCTTCGGGACC  
AACTTGCCCTCAGCTCGGACAACCTTCCTCCACTGGCCCCCTCTAACTCTGAACATCCGCAGCCCCG  
TCTGGACCCCTAGGTCTAATGACTTGGCAAGGGTTCTCTGAAGCTCAGCGTGCCTCCATCAGATG  
GCTTCCCACCTGCAGGAGGTTCCTGCAGTGCAGAGGTGGCCTCCATCGTGGGGGCTGCCTGCCATG  
GATTCTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGGCTGAGGACCGCCTGGGGGA  
AGCGCTGCCTGAAGAACTCTCTTACCTCTCCAGTGTGCGGCCCTCGCTCCGGGCAGTGGCCCTT  
TGCTTGGGGAGTCTTCTCCCGATGCCACAGGCCCTCTCACCTGAGGCTTCACTCCTCCACCAGGAC  
TCGGAGTCCAGACGACTGCCCCGTTCTAATTCAGTGGGAGCCGGGGGAAAAATCCTTTCCCAACG  
CCCTCCCTGGTCTCTCATCCACAGGGTTCTGCCTGATCACCCCTGGGGTACCCTGAATCCCACTG  
TGTCTGGGGAGGTGGAGGCCCTGGGACTGGTTGGGGAACGAGGCCCATGCCACACCTGAGGGA  
ATCTGGGGTATCAATAATCAACCCCCAGGTACCAGCTGGGGAAATATTAATCGGTATCCAGGAGG  
CAGCTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGGAATATTAATCGGTATCCAGGAG  
GCAGCTGGGGGAATATTCATCTATACCCAGGTATCAATAACCCATTTCTCCTGGAGTTCTCCGC  
CCTCCTGGCTCTTCTTGAACATCCCAGCTGGCTTCCCTAATCCTCCAAGCCCTAGGTTGCAGTG  
GGGCTAGAGCACGATAGAGGGAACCCAACATTGGGAGTTAGAGTCTGCTCCCGCCCCCTTGCTG  
TGTGGGCTCAATCCAGGCCCTGTAAACATGTTTCCAGCACTATCCCCACTTTTCAGTGCCTCCCC  
TGCTCATCTCCAATAAAATAAAAGCACTTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA

## **FIGURE 64**

MQGRVAGSCAPLG LLLVCLHLPGLFARSIGVVEEKVSQNFGTNLPQLGQPSSTGPSNSEHPQPAL  
DPRSNDLARVPLKLSVPPSDGFPFAGGSAVQRWPPSWGLPAMDSWPPEDPWQMAAAAEDRLGEA  
LPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRLPRSNSLGAGGKILSQRP  
PWSLIHRVLPDHPWGTLPNPSVSWGGGGPGTGWGTRPMPHPEGIWGINNQPPGTSWGNNINRYPGGS  
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPPGVLRPPGSSWNIPAGFPNPPSPRLQWG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Casein kinase II phosphorylation sites.**

amino acids 56-59, 155-158

**N-myristoylation sites.**

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,  
259-264, 269-274, 270-275, 280-285, 281-286, 305-310

## **FIGURE 65**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTC  
TGGGCTGCCCCCTTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGA  
CTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAA  
TTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCTCCACCATGC  
AAGATCTCAACACCATGTTGTCTGCAACACATGACAGCCATTGAAGCCTGTGTCTTCTTGGCCC  
GGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTTCAGCAGGCCCCCACCTC  
CTGAGTGGCAATAAATAAAATTCGGTATGCTG

## **FIGURE 66**

MGSGPLVLLLLTLGSSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCLLLHLPSTSVTL  
HHARSQHHVVCNT

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 37-41

N-myristoylation sites.

amino acids 15-21, 19-25, 60-66

## FIGURE 67

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCGGGC  
CAGGTGCCCCGTCGCAGGTGCCCCTGCCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAGCCCC  
TTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCGGGCTGGGGCTGCTTCTGGCG  
CTGGGCCTGCCGTTCTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACAGACCACTTCTGC  
AAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATGGCAACCTGCGTCCGG  
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTCCTGGCTGTGGGGCTG  
GCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCCAGTAGCGA  
GGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCTCAGGACTCCAAGGAGACGGTGCAGGGCT  
GCCTGCCCATCTAGGTCCCCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAA  
GGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAA  
AGACTCTGCCCCTGAGGTCAAGAGAGGATGGGGCTATTCACCTTTTATATATTATATAAAATTAG  
TAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

## **FIGURE 68**

MANPGLGLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSSSTSSSSDGNLRPEAITAIIVVFS  
LLAALLLAVGLALLVRKLRKQRTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

### **Important features:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domain:**

amino acids 56-80

#### **N-glycosylation site.**

amino acids 36-40

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 86-90

#### **Tyrosine kinase phosphorylation site.**

amino acids 86-94

#### **N-myristoylation sites.**

amino acids 7-13, 26-32



## FIGURE 69

GCCAGGAATAACTAGAGAGGAACAATGGGGTTATTTCAGAGGTTTTGTTTTCTCTTAGTTCTGTGCCTGCTGCACCAG  
 TCAAATACTTCCTTCATTAGCTGAATAAATATGGCTTTGAAGATATTGTCATTGTTATAGATCCTAGTGTGCCAGAA  
 GATGAAAAAATAATTGAACAAATAGAGGATATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGA  
 TTTTTTTTCAAAAATGTATCTATATTAATTCTTGAGAATTGGAAGGAAAAATCCTCAGTACAAAAGGCCAAAACATGAA  
 AACATAAACATGCTGATGTTATAGTTGCACCACCTACACTCCAGGTAGAGATGAACCATACCAAGCAGTTTACA  
 GAATGTGGAGAGAAAGCGAATACATTCACTTCACCCCTGACCTTCTACTTGGAAAAAACAAAATGAATATGGACCA  
 CCAGGCCAACTGTTTTGTCCATGAGTGGGCTCACCTCCGGTGGGGAGTGTTTGATGAGTACAATGAAGATCAGCCTTTC  
 TACCGTGCTAAGTCAAAAAAATCGAAGCAACAAGGTGTTCCGCAGGTATCTCTGGTAGAAATAGAGTTTATAAGTGT  
 CAAGGAGGCAGCTGTCTTAGTAGAGCATGCAGAATTGATTCTACAACAAACTGTATGGAAAAGATTGTCAATTCCTT  
 CCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTTATGCAAAGTATTGATTCTGTTGTTGAATTTTGTAAACGAA  
 AAAACCCATAATCAAGAAGCTCCAAGCCTACAAAACATAAAGTGCAATTTTGAAGTACATGGGAGGTGATTAGCAAT  
 TCTGAGGATTTTAAAAACACCATACCCATGGTGACACCACCTCCTCCACCTGTCTTCTCATTGCTGAAGATCAGTCAA  
 AGAATTGTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGGTAAGGACCCCTAAATCGAATGAATCAAGCAGCA  
 AAACATTTCCCTGCTGCAGACTGTTGAAAATGGATCCTGGGTGGGGATGGTTCACTTTGATAGTACTGCCACTATTGTA  
 AATAAGCTAATCCAAATAAAAAGCAGTGATGAAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGA  
 ACTTCCATCTGCTCTGGAATTAATATGCAATTTAGGTGATTGGAGAGCTACATTCCCAACTCGATGGATCCGAAGTA  
 CTGCTGCTGACTGATGGGGAGGATAACACTGCAAGTTCTTGATTGATGAAGTGAACAAAGTGGGGCCATTGTTCA  
 TTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAATAGAGATGAGCAAGATAACAGGAGGAAGTCATTTTATGTT  
 TCAGATGAAGCTCAGAACAATGGCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAATCTGATCTCTCCAGAG  
 TCCCTTCAGCTCGAAAGTAAGGATTAACACTGAATAGTAATGCCCTGGATGAACGACACTGTCATAATTGATAGTACA  
 GTGGGAAGGACACGTTCTTTCTCATCACATGGAACAGTCTGCCTCCAGTATTTCTCTCTGGGATCCAGTGGAAACA  
 ATAATGAAAAATTTACAGTGGATGCAACTTCCAAAATGGCCTATCTCAGTATTCAGGAACTGCAAGGTGGGCACT  
 TGGGCATACAATCTTCAAGCCAAAGCGAACCCAGAAACATTAACTATTACAGTAACCTCTCGAGCAGCAAAATCTTCT  
 GTGCCCTCAATCACAGTGAATGCTAAAATGAATAAGGACGTAAACAGTTTCCCGAGCCCAATGATTGTTTACGCGAA  
 ATTCTACAAGGATATGTACCTGTTCTTGGAGCCAAATGTGACTGCTTTCATTGAATCACAGAATGGACATACAGAAGTT  
 TTGGAACCTTTTGGATAATGGTGCAGCGCTGATTCTTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATAT  
 ACAGAAAAATGGCAGATATAGCTTAAAAGTTTCGGGCTCATGGAGGAGCAAACTGCCAGGCTAAATTTACGGCCTCCA  
 CTGAATAGAGCCGCTACATACCAGCTGGGTAGTGAACGGGGAAATTGAAGCAAAACCCGCAAGACCTGAAATTGAT  
 GAGGATACTCAGACCACCTTGGAGGATTTACGCCGAACAGCATCCGGAGGTGCATTTGTGGTATCACAGTCCCAAGC  
 CTTCCCTTGCTGACCAATACCCACCAAGTCAAATCACAGACCTTGATGCCACAGTTCTGAGGATAAGATTATCTT  
 ACATGGCAGCAGCAGGAGATAATTTTGTGTTGGAAAAGTTCAACGTTATATCATAAGAATAAGTGCAAGTATCTT  
 GATCTAAGAGACAGTTTGTGATGCTCTTCAAGTAAATACTACTGATCTGTACCAGGAGGCAACTCCAAGGAA  
 AGCTTTGCATTTAAACAGAAAATATCTCAGAAAGAAATGCAACCCACATATTTATTGCCATTAAGATATAGATAAA  
 AGCAATTTGACATCAAAAGTATCCAACATGCAAGTAACCTTTGTTTATCCCTCAAGCAAACTCTGATGACATTGAT  
 CCTACACCTACTCCTACTCCTACTCCTACTCCTGATAAAAGTCATAATTCTGGAGTTAATATTTCTACGCTGGTATTG  
 TCTGTGATTGGGTCTGTTGTAATTTGTTAACTTTATTTTAAAGTACCACCATTTGAACCTTAACGAGAAAAAATCTTC  
 AAGTAGACCTAGAAGAGAGTTTTAAAAACAAAACAAATGTAAGTAAAGGATATTTCTGAATCTTAAATTCATCCCAT  
 GTGTGATCATAAACTCATAAAAATAATTTTAAAGTGTCCGAAAAGGATACCTTTGATTAAATAAAAACACTCATGGATA  
 TGTAAAACTGTCAAGATTAATAATTAATAGTTTCATTATTTGTTATTTTATTGTAAGAAATAGTGATGAACAAAG  
 ATCCTTTTTTCTACTGATACCTGGTTGTATATTTTGTGATGCAACAGTTTCTGAAATGATATTTCAAATTCATCAA  
 GAAATTAATAATCATCTATCTGAGTAGTCAAAATACAAGTAAAGGAGAGCAATAAACCAACATTTGGAAAAA  
 AA

## **FIGURE 70**

MGLFRGFVFLVLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIIEQIEDMVTASTYLFE  
ATEKRFFFKNVSILIPENWKENPQYKRPKHENHKKHADVIVAPPTLPGRDEPYTKQFTECGEKGEY  
IHFTPDLLLKGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCISAGISGRN  
RVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDQVTEKASIMFMQSIDSVVEFCNEKTHNQEAP  
SLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLKISQRIVCLVLDKSGSMGGKDRNLNR  
MNQAAKHFLLOTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGLPTYPLGGTSICSGIK  
YAFQVIGELHSQLDGSEVLLLTGDGEDNTASSCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGG  
SHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFL  
ITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSR  
AANSSVPPITVNAKMNDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGA  
GADSFKNDGVYSRYFTAYTENGRYSLKVRAGGANTARLKLRLPPLNRAAYIPGWVVNGEIEANPP  
RPEIDEDTQTTLEDFSRASGGAFVVSQVPSLPLPDQYPPSQITDLDATVHEDKIIILTWTAPGDN  
FDVGKVQRYIIRISASILDRLDSFDDALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAI  
KSIDKSNLTSKVSNIAQVTLFIPQANPDDIDPTPTPTPTPTDKSHNSGVNISTLVLSVIGSVVI  
VNFILSTTI

### **Signal peptide:**

amino acids 1-21

### **Putative transmembrane domains:**

amino acids 284-300, 617-633

### **Leucine zipper pattern.**

amino acids 469-491, 476-498

### **N-glycosylation site.**

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,  
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

## FIGURE 71

CTCCTTAGGTGGAAACCTGGGAGTAGAGTACTGACAGCAAAGACCGGAAAGACCATACGTCCCCGGGCAGGGGTGA  
CAACAGGTGTCTCTTTTGTCTCGTGTGTGGCTGCCTTCTATTCAAGGAAAGACGCCAAGGTAATTTTGACCCA  
GAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCCAAGTTATGCCAGGATTTACTAGAGAGTGTCA  
ACTCAACCAGCAAGCGGCTCCTTCGGCTTAACTTGTGGTTGGAGGAGAGAACCTTTGTGGGGCTGCGTTCTCTTAGCA  
GTGCTCAGAACTGACTTGGCTGAGGGTGGACCAGAAAGAAAGGTCCCTCTTGTCTTGGCTGCACATCAGGAA  
GGCTGTGATGGGAATGAAGGTGAAACTTGGAGATTTCACTTCAGTCATTGCTTCTGCTGCAAGATCATCTTTAA  
AGTAGAGAACTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATGCAAGCAGCTC  
CGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCCAGGGAAGCCCTTCCGTGGGGGGCCCCGGCTTTGAGGGATGCC  
ACCGGTTCTGGACGCATGGCTGATTCCTGAATGATGATGGTTCCGCCGGGGGCTGCTTGCCTGGATTTCCCGGGTGGTG  
GTTTGTGTGTCTCTCTGTCTGTCTATCTCTGTCTGTACATGTTGGCTGCACCCAAAAGGTGACGAGGAGCAG  
CTGGCACTGCCAGGGCCAAACAGCCCCAGGGGAAGGAGGGTACCAGGCCGCTCCTTCAGGAGTGGGAGGAGCAGAC  
CGCAACTACGTGAGCAGCCTGAAGCGGCAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGAGCAGCTCAG  
AATGGGCACTACCAAGCCAGCGATGCTGCTGGCCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAGGCCGACCTC  
CTGGCCTTCTCTGCATCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGGCCACAGAGTATGCAAGCAGTG  
CCTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGGCCTTACCCGCCACCCCGAGGAGAAGCCTGTG  
AGGAAGGACAAGCGGGATGAGTTGGTGGAGGCCATTGAATCAGCCTTGGAGACCTGAACATCTGCAAGAGAACGAC  
CCCAATCACCGTCTTACACGGCCTCTGATTTATAGAAGGGATCTACCGAACAGAAAGGGACAAAGGGACATTGTAT  
GAGCTCACCTTCAAAGGGGACCAACACGAATTCAAACGGCTCATCTTATTTGACCATTCAGCCCCCATGAAA  
GTGAAAAATGAAAAGCTCAACATGGCCAACACGCTTATCAATGTTATCGTGCCTCTAGCAAAAAGGGTGGACAAAGTTC  
CGGCAGTTTCATGCAGAAATTCAGGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCTCACTGTTGTTTACTTTGGG  
AAAGAAGAAATAAATGAAGTCAAAGGAATACTTGAAAACACTTCCAAAGCTGCCAACTTCAGGAACCTTACCTTCATC  
CAGCTGAATGGAGAATTTCTCGGGGAAAGGCACTTGATGTTGGAGCCCGCTTCTGGAAGGGAAGCAACGTCCTTCTC  
TTTTTCTGTGATGTGGACATCTACTTCACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGGAAGAG  
GTATTTTATCCAGTTCTTTTTCAGTCAGTACAATCCTGGCATAATATACGGCCACCATGATGCAGTCCCTCCCTTGGAA  
CAGCAGCTGGTCATAAAGAAGGAACTGGATTTTGGAGAGACTTTGGATTGGGATGACGTGTGAGTATCGGTGACAC  
TTCAATCAATATAGGTGGGTTTATCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCACCTTTATCGCAAGTATCTC  
CACAGCAACCTCATAGTGGTACGGACGCTGTGCGAGGACTCTCCACCTCTGGCATGAGAAGCGCTGCATGGACGAG  
CTGACCCCGGAGCAGTACAGATGTGCATGCAAGTCCAAGGCCATGAACGAGGCATCCACGGCCAGCTGGGCATGCTG  
GTGTTTCAGGCACGAGATAGAGGCTCACCTTCGCAACAGAAACAGAAAGCAAGTAGCAAAAAACATGAACTCCAGAG  
GAAGGATTGTGGGAGACACTTTTCTTTCTTTTGAATTAAGTGGCTGCAACAGAGAAAAGACTTCCATAAA  
GGACGACAAAAGAAATGGACTGATGGGTGAGAGATGAGAAAGCCTCCGATTTCTCTCTGTTGGGCTTTTACAAACAGA  
AATCAAAATCTCCGCTTTCCTGCAAAAGTAACCCAGTTGCACCTGTGAAGTGTCTGACAAAGGCAGAAATGCTTGTG  
AGATTATAAGCCTAATGGTGTGGAGGTTTGTATGGTGTTTACAATACACTGAGACCTGTTGTTTTGTGTGCTCATTGA  
AATATTCATGATTTAAGAGCAGTTTGTAAAAAATTCATTAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGA  
GCCTATCAGCAGGGCTCTAGTTTCTAGGAATGCTAAAAATATCAGAAGGCAGGAGAGGAGATAGGCTTATATGATACT  
AGTGAGTACATTAAGTAAATAAATGAGCAGAGAAAGAAAGAAACCATAAATATCGTGTGATATTTTCCCCAAGAT  
TAACCAAAATAATCTGCTTATCTTTTGGTGTCTCTTTAACTGTCTCCGTTTTTTCTTTTATTTAAAAATGCACCT  
TTTTTTCCTTGTGATTATAGTCTGCTTATTTAATTACCACTTTGCAAGCCTTACAAGAGAGCAAGTTGGCCTAC  
ATTTTATATTTTAAAGAGATACTTTGAGATGCATTATGAGAACTTTCAGTTCAAAGCATCAAATTGATGCCATAT  
CCAAGGACATGCCAATGCTGATCTGTGAGGCACTGAATGTCAGGCATTGAGACATAGGGAAGGAATGGTTGTACT  
AATACAGACGTACAGATACTTTCTCTGAAGAGTATTTTCGAAGAGGAGCAACTGAACACTGGAGGAAAGAAATGAC  
ACTTCTGCTTTACAGAAAAGGAACTCATTGAGACTGGTGATATCGTGATGTACCTAAAAGTCAGAAACCACATTTT  
CTCCTCAGAAAGTAGGGACCGCTTCTTACCTGTTTAAATAAACCAAGTATACCGTGTGAACCAACAATCTCTTTTC  
AAAACAGGGTGTCTCCTTGGCTTCTGGCTCCATAAGAAGAAATGGAGAAAATATATATATATATATATATTGT  
GAAAGATCAATCCATCTGCCAGAATCTAGTGGGATGGAAGTTTGTGCTACATGTTATCCACCCAGGCCAGGTGGAAG  
TAACTGAATATTTTAAATTAAGCAGTTTACTCAATCACAAGATGCTTCTGAAAATTGCATTTTATTACCATTT  
CAAATATTTTAAAAATAAATACAGTTAATACATAGAGTGGTTTCTTCAATCATGTGAAAATATTAGCCAGCAGCAG  
ATGCATGAGCTAATTATCTTTGAGTCTTGTCTGTTTGTCTCACAGTAAACTCATGTTTAAAGCTTCAAGAAC  
ATTCAAGCTGTTGGTGTGTTAAAAATGCATTGTATTGATTGTACTGGTAGTTTATGAAATTTAATTAACACAGG  
CCATGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTGTGGATATGAA

## **FIGURE 72**

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPGKEGYQAVLQEW  
EQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQV  
AEVNAGVKLATEYAAVFPDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALET  
ENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVNEK  
TLINVIPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVGILENTSKAANFR  
TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFY  
NPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDV  
KYLHSNLIVVRTPVRLGHLWHEKRCMDLTPEQYKMCMSKAMNEASHGQLGMLVFRHEIEA  
RKQKQKTSSKKT

### **Important features:**

#### **Signal peptide:**

amino acids 1-27

#### **N-glycosylation sites.**

amino acids 315-319, 324-328

#### **N-myristoylation sites.**

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

#### **Amidation site.**

amino acids 377-381



## **FIGURE 74**

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPLPALQ  
PHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGSEHQINSEAT  
FAELHIVHYSDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP  
FNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKLLV  
QNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLNRKS  
VVFTSAQATTEA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

## FIGURE 75

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGTGTC  
TCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAAATGTCCTACA  
ATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTTTCATCACAA  
ATTGGCCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCTGACAGCTCC  
AGAGAAGTGAAGAGAAATCCAGAAGACCTTCTGTTTCCATGCAACAAATATACTCCAATCTGA  
AGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAACCAC  
ACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCTTTCGTCCC  
AGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGATCAATCAT  
CAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGTGTTCCTTTTT  
TCTGTGATGGGCTATTCCATCTACCGATATATCCACGTGGCAAAGAGAAACACCCAGCAAATTT  
GATTTTGATTTATGGAATGAATTTGACAAAAGATTCTTTGTGCGCTGCTGAAAAATCGTGATTA  
ACTTTATCACCCCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGATATGAGTTTACTGGGA  
AAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGA  
GGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAG  
AAAACACGGAAGGTACTTCTCTCAGCCAGCAAGAGTCCCTCAGCAGAAACAAATACCCCGGATAAA  
ACAGTCATTGAATATGAATATGATGTGAGAACCCTGACATTTGTGCGGGGCCTGAAGAGCAGGA  
GCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAG  
TCTTGGGCCCCGAAACGTTACAGTACTCATACACCCCTCAGTCCAAGACTTAGACCCCTGGCG  
CAGGAGCACACAGACTCGGAGGAGGGGCCGAGGAAGAGCCATCGACGACCTGGTCGACTGGGA  
TCCCCAACTGGCAGGCTGTGTATTCTTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCG  
AGCCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGCT  
CCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGTATA  
TGTGCAGATGGAAGAACTGATGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAACAAGTGAG  
TCACCCCTTTGATCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTGAGTGT  
CTGTGAGAATTACTTATTTCTTTCTCTATTCTCATAGCACGTGTGTGATTGGTTCATGCATGTA  
GGTCTCTTAACAATGATGGTGGGCTCTGGAGTCCAGGGGCTGGCCGTTGTCTATGCAGAGAA  
AGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGGTGGGTGT

## **FIGURE 76**

MSYNGLHQRVFKELKLLTLCSISSQIGPPEVALTTDEKSISSVVLTAPEKWKRNPEDLPVSMQQIY  
SNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLK  
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGKEKHPANLILYIGNEFDKRFFVPAEK  
IVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFC  
DSEENTEGTSLTQQESLSRTIPPDKTVIEYDYVRTTDICAGPEEQELSLQEEVSTQGTLLLSQA  
ALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLVDWDPQTGRLCIPSLSSFDQDS  
EGCEPSEGDGLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426



## FIGURE 77

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACAC  
CTGGGAAGATGCGCCGCGCCGTGGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATC  
CAAGCCACCCTCAGTCCCAGTGCAGTTCTCATCCTCGGCCAAAAGTCATCAAAGAAAAGCTGAC  
ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGC  
GGGAAAAGCCAGCCGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACCGTCCTGAAGCACATC  
ATCTGGCTGAAGGTATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCCCTCGGCCAATGACCA  
GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCCTGGTCAAGACCA  
TCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGC  
CCCACCCGCTGGTCCTCAGTGAAGTGTGCCACCAGCCATGGGAGCCTGCGCATCCAAGTGTGTA  
TAAGCTCTCCTTCCTGGTGAACGCTTAGCTAAGCAGGTATGAACCTCCTAGTGCCATCCCTGC  
CCAATCTAGTGAAAACAGCTGTGTCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGAC  
CTCCTGCAGCTGGTGAAGGTGCCCATTTCCCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTA  
TCCTGCCATCAAGGGTGACACCATTAGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAA  
AGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCTTGACAATGCCACCCTGGACAACATCCCG  
TTCAGCCTCATCGTGAGTCAGGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA  
ATTCATGGTCTGTGGACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGC  
TGATCAATGAAAAGGTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGAC  
ACTCCCGAGTTTTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGTGGAAGTGT  
TCCCTCCAGTGAAGCCCTCCGCCCTTGTTCACCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGT  
TTTACACCAAAGGTGACCAACTTATACTCAACTGAATAACATCAGCTCTGATCGGATCCAGCTG  
ATGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA  
CTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTGATTGGTGAAGG  
CCTTGGGATTGAGGCAGCTGAGTCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCC  
TTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGG  
GTCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTG  
CCTGTGAAAAA

## **FIGURE 78**

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQLPLLSAMREK  
PAGGIPVLGSLVNTVLKHI IWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVE  
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL  
VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYLGAKL LDSQGKVT  
KWFNNSAASLTMTLDNIPFSLIVSQDVVKA AVAVLSPEEFMVLLDSVLPESAHLKSSIGLIN  
EKAADKLGSTQIVKILTQDTP EFFIDQGHAKVAQLIVLEVFPSS EALRPLFTLGIEASSEAQFYT  
KGDQLILNLNNISSDRIQLMNSGIGWFPDVLKNIITEIIHSILLPNQNGKLRSGVPVSLVKALG  
FEAAESSLT KDALVLT PASLWKPSSPVSQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457

## FIGURE 79

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC  
TTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCT  
CTTGGCCTCCAACCTTGTTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGTTGCCAT  
GCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAGCAGTTGGCTTCT  
CCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGACATCTATAGC  
ACCCCTTCTGGGCCTGCCCCTGACATCCAGGCTGCCCAGGCCATGATGGTGACATCCAGTGCAAT  
CTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCCAGGAATCCC  
GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTCATCCTTGAGGCCCTCCTGGGATTC  
ATTCTGTGCTGGAATCTTCATGGGATCCTACGGGACTTCTACTCACCCTGGTGCCTGACAG  
CATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTCTTCCCTGTTCTCCCTGATAG  
CTGGAATCATCCTCTGCTTTTCTGCTCATCCCAGAGAAATCGCTCCAACCTACTACGATGCCTAC  
CAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGA  
GTTCAATTCCTACAGCCTGACAGGGTATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGGTGGCTG  
GGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGT  
GTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGG  
GCTAGTGTAAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCC  
TCACCTTGCTGCTCCCCTGCCCTAAGTCCCCAACCCCTCAACTTGAAACCCCATTCCTTAAGCCA  
GGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACA  
TCCCCTGACTGACCCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATT  
GCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTC  
CCTCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCCTCTGTTATGACTCCACAGTGTCCA  
GACTAATTTGTGCATGAAGTGAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATG  
CAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

## **FIGURE 8o**

MASLGLQLVGYILGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCD  
IYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGL  
LGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLSLIAGIILCFSCSSQRNRSNYY  
DAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

## FIGURE 81

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTC  
CCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTTCCTGCCCTCCTTTCCT  
GCCCACCGCTGCTTCTTGGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGG  
GTTGATCTGTGGCCCTGTGCCCTCCGTGTCTTTTCGTCTCCCTTCCTCCCGACTCCGTCCCGG  
ACCAGCGGCCTGACCCTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCTCTCCTCCTTGCTGGGA  
CTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCAGACATGTTCTGCCTTTT  
CCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACTTGAGGCCACAAGGCCTGATGT  
ACTGCCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCT  
GTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACAC  
TCCCTCTGGACTCCGGGCCCCACCAAAGTCTGCCAGCACAAACGGGACCATGTACCAACACGGAG  
AGATCTTCAGTGCCCATGAGCTGTTCCCTCCCGCTGCCCAACCAAGTGTGTCTCTGCAGCTGC  
ACAGAGGGCCAGATCTACTGCGGCTCACAACCTGCCCCGAACCAAGGCTGCCAGCACCCCTCCC  
ACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAAGAGGACA  
GTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAG  
AGAGGCCCGGGCACCCAGCCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTT  
CAGACCCAAGGGAGCAGGCAGCACAACTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCT  
GTGTGCATGGCGGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGC  
CCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC  
CACCGAGTACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCAGAGG  
ACAAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTC  
CTCGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGGC  
CTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAACTGAGGCTCAGAGAG  
GTGAAGTACCTGGCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAG  
GAAGCAAGACTTCCAGAAAGAGGCACAGCACCTCCGACTGCTCGCTGGCCCCACGAAGGTCAT  
GGAACGTCTTCTAGCCCAGACCCTGGAGCTGAAGGTACGGCCAGTCCAGACAAAGTGACCAAG  
ACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATGTTGTTATTATATATTAATAAA  
TAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 82**

MVPEVRVLSSLLGLALLWFPLDSHARAPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSE  
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELF  
PSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR  
HPQDPCSSDAGRKRGPPTAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKHKACVHGGKTYS  
HGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTTEYPCRHEKVAGKCKICPEDKADPGHSE  
ISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH  
SQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSDPGAEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

## FIGURE 83

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCAGCGAGAGCCTCTCC  
GTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTCTAATCCATCCGTCACCTCTCCTGTCA  
TCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTCTCATGCTCAGTTTGTTCTGAGTC  
TCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTGGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAG  
GACGCAGCATTCTCCTGTTCCTGTCTCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGG  
CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATC  
AAGGCAGGACAAAACCTGGTGAAGGATTCTATTGGGGAGGGGGCGCATCTCTCTGAGGCTGGAAAAATTACT  
GTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCATCTGGGAGCT  
ACAGGTGTGAGCACTGGGCTCAGTTCTCTCATTTCATCACGGGATATGTTGATAGAGACATCCAGCTAC  
TCTGTCACTCCTCGGCTGGTTCCTCCCGGGCCACAGCGAAGTGGAAGGTCCACAAGGACAGGATTTGTCC  
ACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAA  
CGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAG  
GAGATACCTTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTA  
TTTTTTGGCATTGTGGACTGAAGATTTTCTTCTCCAAATTCAGTGGAAAAATCCAGGCGGAACTGGACTG  
GAGAAGAAAGCACGGACAGGCAGAAATTGAGAGACGCCCCGAAACACGCAGTGGAGGTGACTCTGGATCCAG  
AGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAACTGTAAACCCATAGAAAAGCTCCCCAGGAGGTG  
CCTCACTCTGAGAAGAGATTACAAGGAAGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCAGGGAAACATTA  
CTGGGAGGTGGACGGAGGACACAATAAAGGTGGCGCTGGGAGTGTGCCGGATGATGTGGACAGGAGGA  
AGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTT  
ACATTAAATCCCCGTTTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTCTGGACTA  
TGAGTGTGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTGCGTTTG  
AAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACCTCCCATAGTCATCTGC  
CCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGCCAAAGGCCTCTGCAATCCCAGAGACAAGCAACAG  
TGAGTCTCTCTCACAGGCAACCACGCCCTTCTCCCCAGGGTGAAATGTAGGATGAATCACATCCCACAT  
TCTTCTTTAGGGATATTAAGGTCTCTCTCCAGATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCA  
GATGAAGGGGACTGGCCTGTCCACATGGGAGTCAGGTGTCTATGGCTGCCCTGAGCTGGGAGGGAAGAAGG  
CTGACATTACATTTAGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAATACCACCTCTCAGGTGAAG  
AACCGTCAGGAATCCCATCTCACAGGCTGTGGTGTAGATTAAAGTAGACAAGGAATGTGAATAATGCTTAG  
ATCTTATTGATGACAGAGTGTATCCTAATGTTTGTTCATTATATTACACTTTCAGTAAAAAAA

## **FIGURE 84**

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCLSPKTNAEAMEVRFFRGQFSSVVH  
LYRDGKDQPFMQMPQYQGR TKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQKAIWELQ  
VSALGSVPLISITGYVDRDIQLLCQSSGWFP RP TAKWKGPQGDLSTDSRTNRDMHGLFDVEISL  
TVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK  
FQWKIQAE LDWRRKHGQAE LR DARKHAVEVT LDPETAHPKLCVSDLKTVTHRKA PQEVP HSEKRF  
TRKSVVASQS FQAGKHYWEVDGGHNKRWRVGVC RDDVDRRKEYVTLS PDHGYWVLR LN GEHLYFT  
LNPRFISVFPRTPTPKIGVFLDYECGTISFFNINDQSLIYTLTCRFEGLLRPYIEYPSYNEQNGT  
PIVICPVTQESEKEASWQRASAI PETSNSSESSQATT PFLPRGEM

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255



## FIGURE 85

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCCCCCT  
GCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTTCCGTGA  
CGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCATGGCTGGATT  
TACCCTGGCCCAGTAGTTTCATGGCTACTGGTTCGGGAAGGGGCCAATACAGACCAGGATGCTCC  
AGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACCGATTCCACCTCCTTG  
GGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGAAGAAGTGATGCGGGGAGA  
TACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCACCGGCTCTCTGTGAA  
TGTGACAGCCTTGACCCACAGGCCAACATCCTCATCCAGGCACCCTGGAGTCCGGCTGCCCCC  
AGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAGGGGACACCCCTATGATCTCCTGGATA  
GGGACCTCCGTGTCCCCCTGGACCCCTCCACCACCCGCTCCTCGGTGCTCACCCCTCATCCCACA  
GCCCCAGGACCATGGCACCAGCCTCACCTGTGAGGTGACCTTCCCTGGGGCCAGCGTGACCACGA  
ACAAGACCGTCCATCTCAACGTGTCTACCCGCTCAGAACTTGACCATGACTGTCTTCCAAGGA  
GACGGCACAGTATCCACAGTCTTGGGAAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCT  
GCGCCTGGTCTGTGCACTTGATGCACTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGA  
GAGGCCTGACCCTGTGCCCTCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCAC  
CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCT  
GAACGTCTCCCTGCAGAGCAAAGCCACATCAGGAGTGACTCAGGGGTGGTGGGGGAGCTGGAG  
CCACAGCCCTGGTCTTCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAA  
TCGGCAAGGCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTGAGGGTTC  
AGCCTCTCAGGGGCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAG  
CTTCTGCCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGTG  
AAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCCACAG  
ATGAGAACTGCAGAGACTCACCCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGAGAAGTCA  
GAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATG  
TGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCC  
TCCCTTTTATTTTTTAACTAAAAGACAGACAAATTCCTA

## **FIGURE 86**

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSYPSHGWYIPGPVVHGYWFREG  
ANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNY  
KHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSVPWACEQGTPPMISWIGTSVSPLDPSTTRS  
SVLTLLIPQPDHGTSLTCQVTFPGASVTTNKTVHLNVSYPPQNLTMTVFQGDGTVSTVLGNGSSL  
SLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAAEFTCRAQNP  
LGSQQVYLVNLSLQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGDGTGIE  
DANAVRGASASQGPLEPWAEDSPPDQPPASARSSVGEDELQYASLSFQMKPWDSRGQEATDTE  
YSEIKIHR

### **Signal peptide:**

amino acids 1-15

### **Transmembrane domain:**

amino acids 351-370

## FIGURE 87

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTAC  
CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTC  
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGT  
TCTTCGCTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCATTTGA  
TGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCTGTGACATGACCTCTG  
GGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGGAAGTGCACGGTG  
GGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAACTGGGC  
CAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCTGGCTACT  
ACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCCAATAAGTCCCCATGCAGCACTGG  
AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCT  
GTTTGGCATCTACCAGAAATATCCAGTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGGCC  
CGGTGATCCCTGTGGTCTATGATTTTGGCGACGCCAGAAAACAGCATCTTATTACTCACCTTAT  
GGCCAGCGGGAATTCAGTGCGGGATTTGTTCACTTCAGGGTATTTAATAACGAGAGAGCAGCCAA  
CGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG  
GATACTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATAT  
GGAACATCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG  
TTGAGAGTTTTGTGGGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAA  
CAACTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGA  
AAAAAA

## **FIGURE 88**

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI  
YQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAAT  
SDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYG  
EGKCWTDNGPVIPIVVYDFGDAQKTASYISPYGQREFTAGFVQFRVFNNERAANALCAGMRVTGCN  
TEHHCIGGGGYFPEASPOQCDFSGFDWSGYGTHVGYSRSSREITEAAVLLFYR

**Important features:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation site.**

amino acids 163-167

**Glycosaminoglycan attachment sites.**

amino acids 74-78, 289-293

**N-myristoylation sites.**

amino acids 76-82, 115-121, 124-130, 253-259, 292-298

## FIGURE 89

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGAGAC  
CGCCGCCCTTGTCCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCCTGACG  
CTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACATACAGGCCTG  
CCTGCCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTACAGCTGGTGGCCGCGCTCT  
CTGTCAACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCTCTCAGGAGTCTCCATGTTCAAC  
AGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGCCCTGTCCTTCTTCAT  
ATTTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTTGTCTTCTGCAGTGCCCTTCCAGCTG  
TCACTGAAATGGCTTTATTTCGTACCGTCTTTGGGCTGAAAAAGAAACCCTTCTTGATTACCTTCA  
TGACGGGAACCTAAGGACGAAGCCTACAGGGGAAGGGCCGCTTCGTATTCTGGAAGAAGGAAG  
GCATAGGCTTCGGTTTTCCCCTCGGAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACG  
TCTTGAGTCTGGGATTATCCGCATTGTATTTAGTGCTTTGTAATAAAATATGTTTTGTAGTAACA  
TTAAGACTTATATACAGTTTTAGGGGACAATTAAAAAAAAAAAA

**FIGURE 90**

MGRVSGLVPSRFLTLLAHLVVVITLFSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFA  
VELAGFLSGVMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVTEMALFV  
TVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

## FIGURE 91

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGAC  
TCGCTGCTGCTTCGTGTTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATG  
GTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCT  
CGGAAGCGGGGCCACATCTCACCTAAGTCCCCCCCCATGGCCAATTCCACTCTCCTAGGGCTGCT  
GGCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCCCGAACCACAGCCCCC  
CACCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCCAACATCAAGACGGTG  
GCCCTGAACCTGCTCGTCACAGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTCCACTT  
CCAACACAATGCCACAGGCCAGGGAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAG  
AGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATG  
GAGTGGGAGAAGGTAGAACGGGGCCCGCGACCTCGCTTTGCACCCACGACCCAGCCAAGATCTG  
CTCCCGAGACCACGCTCAGAGCTCAGCCACCTGGAGCTGCTCCCAGCCCTTCAAAGTCGTCTGTG  
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCCAGATTACAACACTAC  
CATAGTGATACCCCCTACTACCCATCTGGGTGACCCGGGGCAGGCCACAGAGCCAGGCCAGGGC  
TGGAAGGACAGGCCTGCCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGGCTC  
AGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG  
AGAAAGGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGG  
AGGAGGAGTGGGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGG  
TCCCCGAGGCCTGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGC  
CCTTGCTTCTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACA  
GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGG  
GCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCTTGTCTGTGCTGAGCATGG  
CATGAGGCTGAAGTGGAACCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTCCAGC  
CAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATG  
GCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCCACAGCCCATC  
CGCGTGCTGTGTGCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCG  
GAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTGACACGGGGTCTCCCGGATCTGGATGGCGC  
CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGCCGAGAGCATGTGCTGGATCTGTTC  
TGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGTGAAACCGCTGATTGCTGACTTT  
TGTGTGAAGAATCGTGTTCTTGGAGCAGGAAATAAAGCTTGCCCCGGGGCA

## **FIGURE 92**

MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL  
LGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTF  
SVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGRRTSLCTHDP  
AKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVC PDYNYHS DTPYYPSG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71



## FIGURE 93

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTCGCC  
CTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGCTTTCTT  
CTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTGGTTTCATGGCAAGAGTCATTATTGACAACA  
AAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTGTCTCTGTCTATATCCAAGAA  
ATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTTGAAGAGTATAAACCC  
AGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGGGCTTTGGAATCATGA  
GTGGAGTATTTTCCTTTGTGAATACCCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCATTTCAT  
GGAGATTCTCCTCAATTCTTCCTTTATTACAGCTTTCATGACGCTGGTCATTATCTTGCTGCATGT  
ATTCTGGGGCATTGTATTTTTTGTGGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTC  
TCCTGACCCACCTGCTGGTGTGACCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCG  
TCAGCATTTATAATCCTGGTGTCTATGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCG  
AAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGAT  
AACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCT  
TTTTCTGAAAATCCCTTTTTCTGGTGGAATTGAGAAAGAAATAAACTATGCAGATA

## **FIGURE 94**

MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDG  
PTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGV  
FSFVNTLSDSLGPPTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVLLT  
HLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKCLLCQDKNFLLYNQSR

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

#### **Glycosaminoglycan attachment site.**

amino acids 120-123

#### **Sodium:neurotransmitter symporter family protein**

amino acids 31-65

## FIGURE 95

AATTTTTCACCAGAGTAAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTCGTG  
GACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTTGTCTTCTAGGATCAAC  
TCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAACTGGCTCCGGATCAGG  
GAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTGATACCATTAAAC  
CAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGGAATGACACCTGGTAC  
CCAGACCCACCCATTGACCCTGGGAGGGTTGAATGTACAACAGCAACTGCACCCACATGTGTTAC  
CAATTTTGTACACAACCTTGGAGCCCAGGGCACTATCCTAAGCTCAGAGGAATTGCCACAAATC  
TTCACGAGCCTCATCATCCATTCTTGTTCCTCCGGGAGGCATCCTGCCCACCAGTCAGGCAGGGGC  
TAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAGGAGCAGGTGTAAATCCTGCCACCCAGG  
GAACCCACGAGGCCGCTCCCAACTCCCAGTGGCACAGATGACGACTTTGCAGTGACCACCCCT  
GCAGGCATCCAAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA  
GTAAGCTGTTTCAAATTTTTTCAACTAAGCTGCCTCGAATTTGGTGATACATGTGAATCTTTATC  
ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTTAGAAGAAATTAATTCTTAATT  
TACCTGAAAATATTCTTGAAATTTCAAGAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAA  
CAATAATTCAATGGATAAATCTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATAT  
TAAAACATATTTGGAAAACCTGGAAA  
AAA

## **FIGURE 96**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM  
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGILSSEE  
LPQIFTSLLIHSLEFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG  
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16

APP ID=10063534

## FIGURE 97

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCTCT  
 CTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCTGTCTTGACCATG  
 GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTCCCAAGGCCAGCCTGC  
 AGAGCTGTCTGTGGAAGTTCAGAAAACTATGGTGGAAATTTCCCTTTATACCTGACCAAGTTGC  
 CGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGTGTGAGGGGACTCAGGCAAGGCAACTGAG  
 GGCCCATTTGCTATGGATCCAGATTCTGGCTTCTGCTGGTGACCAGGGCCCTGGACCCGAGAGGA  
 GCAGGCAGAGTACCAGCTACAGGTCACCTGGAGATGCAGGATGGACATGTCTTGTGGGGTCCAC  
 AGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTGCCCCATTTCTCTCAAGCCATCTAC  
 AGAGCTCGGCTGAGCCGGGGTACCAGGCTGGCATCCCCCTTCTCTTCTTGGGCTTCAGACCG  
 GGATGAGCCAGGCACAGCCAACCTCGGATCTTCGATTCCACATCCTGAGCCAGGCTCCAGCCAGC  
 CTTCCCCAGACATGTTCCAGCTGGAGCCTCGGCTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGC  
 ACCAGCCTTGACCACGCCCTGGAGAGGACCTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGA  
 CCAGGCAGCTCAGGCCACAGGCCACTGCCACCGTGAAGTCTCCATCATAGAGAGCAGCTGGGTGT  
 CCCTAGAGCCTATCCACTGGCAGAGAATCTCAAAGTCTATACCCGACCCACATGGCCCCAGGTA  
 CACTGGAGTGGGGGTGATGTGCATATCACCTGGAGAGCCATCCCCGGGACCCCTTTGAAGTGAA  
 TGCAGAGGGAAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGCCAGGCTGAGTACCTGCTCC  
 AGGTGCGGGCTCAGAAATCCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTG  
 ATGGATGAGAATGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCT  
 CAGTCCACCAGGTACTGAAGTGACTAGACTGTGACAGAGGATGCAGATGCCCCGGCTCCCCCA  
 ATTCCCACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTC  
 CAGGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACAT  
 CCTGCTTCTGGTGTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCAGTGTGAAG  
 TCGAAGTCGCAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACTTCCAGATTGGGCT  
 ATAAGCCTCCCTGAGGATGTGGAGCCCGGACTCTGGTGGCCATGCTAACAGCCATTGATGCTGA  
 CCTCGAGCCCGCTTCCGCTCATGGATTTTGCCATTGAGAGGGGAGACACAGAAGGACTTTTG  
 GCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTTATGAG  
 GCAGCTCCAAGTCATGAGGTGGTGGTGGTGCAGAGTGTGGCGAAGCTGGTGGGGCCAGGCCC  
 AGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGAGTGTGCCACCCCCAAGTTGG  
 ACCAGGAGAGCTACGAGGCCAGTGTCCCATCAGTGCCCCAGCCGGCTCTTTCCTGCTGACCATC  
 CAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCTCCCTAGTCAATGACTCAGAGGGCTGGCT  
 CTGCATTGAGAAATTCCTCGGGGAGGTGCACACCGCCAGTCCCTGCAGGGCGCCAGCCTGGGG  
 ACACCTACACGGTGCTTGTGGAGGCCAGGATACAGCCCTGACTCTTGCCCTGTGCCCTCCCAA  
 TACCTCTGCACACCCCGCCAAGACCATGGCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCT  
 GGCCAGTGGGCACGGTCCCTACAGCTTCACCCTTGGTCCCAACCCACGGTGCACGGGATTGGC  
 GCCTCCAGACTCTCAATGGTTCCCATGCCATACCTCACCTTGGCCCTGCATTGGGTGGAGCCAGT  
 GAACACATAATCCCGTGGTGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCCGAGTGAT  
 CGTGTGTGCTGCAACGTGGAGGGGAGTGCATGCGCAAGGTGGGCCGATGAAGGGCATGCCCA  
 CGAAGCTGTGCGCAGTGGGCATCCTTGTAGGCACCTGGTAGCAATAGGAATCTTCTCATCCTC  
 ATTTTCACCCACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCT  
 GAAGGCGACTGTCTGAATGGGCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAG  
 TCCCCTGGGAGAGAGCCAGCACCCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCCTCA  
 TCTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCAACTT  
 TATGGAAGTCCCATGGGAGTGTCTCCAAATGTCAGGGTGTGTTGCCCAATAATAAAGCCCCAGAGAA  
 CTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

## **FIGURE 98**

MVPAWLWLLCVSVPQALPKAQPAELSVPEVPEYGGNFPLYLTKLPLPREGAEGQIVLSGDSGKAT  
EGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVPHFSQAI  
YRRLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRLGALALSPKG  
STSLDHALERTYQLLVQVKMDGDAQSGHQATATVEVSI IESTWVSLEPIHLAENLKVLYPHHMAQ  
VHWSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQNSHGEDIAAPLELHVL  
VMDENDNVPICPPRDPTVSIPELSPPGTEVTRLSAEDADAPGSPNSHVYQLLSPEPEDGVEGRA  
FQVDPTSGSVTLGVLPILRAGQNILLVLAMDLAGAEGGFSSTCEVEVAVTDINDHAPEFITSQIG  
PISLPEDVEPGTLVAMLTAIDADLEPAFRMLDFAIERGDTEGTFGLDWEPPDSGHVRLRLCKNLSY  
EAAPSHEVVVVVQSVAKLVGPGPGGATATVTVLVERVMPPPKLDQESYEASVPISAPAGSFLLT  
IQPSDPISRTLRFSLVNDSEGWLCIEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALTAPVPS  
QYLCTPRQDHGLIVSGPSKDPDLASGHGPYSFTLGPNPTVQRDWRLQTLNGSHAYLTALHWWEP  
REHIIPVVVSHNAQMWQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGTLLVAIGIFLI  
LIFTHWTMSRKKDPDQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

## FIGURE 99

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCACGCCTG  
AGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTA  
TCTCTTCACCTTCAAGTCCCCTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAGTCTTGGTAC  
ATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAGATGAAGATGCAGAAAGGAAATG  
TTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCCAATGAGACTAGCACC  
TCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCACCAACTCTGGGTCCAG  
TGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGGGGTCA  
GCATAGTCAACCAACTCTGAGTTCATACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAG  
TTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGG  
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACACCCTCCAGTGGGGCCAGCACAGTCAACCAACT  
CTGGGTCCAGTGTGACCTCCAGTGGAGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCC  
AGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCAC  
CAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAA  
CCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACT  
GCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG  
AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACAGCTCCAGTGGGGCCA  
GCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAG  
TCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG  
GGCTAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACT  
CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCAACCAATTCTGAGTCCAGCACACCCTCC  
AGTGGGGCCAAACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAAACAGCCAC  
CAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAA  
CCTCCAGTGGGGTCCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACA  
GCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCTAG  
CACAGTGTCCAGTGGGATCAGCACAGTCAACCAATTCTGAGTCCAGCACAACTCCAGTGGGGCCA  
ACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGA  
ATGCACACAACTTCCCATAGTGCATCTACTGCAGTGAAGTGAAGGCAAAGCCTGGTGGGTCCCTGGT  
GCCGTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCGGCGTGGGGCTCTTTGCTGGGC  
TCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGTCTACCACCT  
CATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCCACAGGCCAG  
GTGGAGTCTTAAGTGGTCTGGAGGAGACAGTATCATCGATAGCCATGGAGATGAGCGGGAGGA  
ACAGCGGGCCCTGAGCAGCCCCGGAAGCAAGTGGCGATTCTTCAGGAAGGAAGAGACCTGGGCA  
CCCAAGACCTGGTTTCTTTTCAATTCATCCAGGAGACCCCTCCAGCTTTGTTTGAGATCCTGAA  
AATCTTGAAGAAGGTATTCCTCACCTTTCTTGCTTTACCAGACACTGGAAGAGAATACTATAT  
TGCTCATTTAGCTAAGAAATAAATACATCTCATTAACACACAGACAAAGAGAAGCTGTGCTTG  
CCCCGGGTGGGTATCTAGCTCTGAGATGAACAGTTATAGGAGAAAACCTCCATGCTGGACTC  
CATCTGGCATTCAAAATCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 100**

MKMQKGNVLLMFGLLLHLEAATNSNETSTSTANTGSSVSSGASTATNSGSSVTSSGVSTATISGS  
SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESSTPSS  
GASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTSSGASTA  
TNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTNGAGTATNSES  
STTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNSDSSTTSS  
GAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNSESSTVSSGASTA  
TNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEASTATNSESSTVSSGISTVTNSES  
STTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVA  
AVGLFAGLFFCVRNLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAPHRPRWSPNWFWRFPVSSI  
AMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532



## FIGURE 101

GGCCGGACGCTCCGCGTTACGGGATGAATTAACGGCGGGTCCGCACGGAGGTTGTGACCCCTA  
CGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTCACAGGTG  
GGAGGCTGGAACATACAGGCTGAAAAACAGAGTGGGTACTCTTCTGGAAGCTGGCAACAAAT  
GGATGATGTGATATATGCAATTCCAGGGGAAGGAAATTGTGGTGCTTCTGAACCCATGGTCAATT  
AACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCTTTGGAATCAT  
GGTGTCATGGAAGGGATTTACTTTTACTGACTCTGTTTTGGGGAAGCTTTTTTGAAGCATTT  
TCATGCTGAGTCCCTTTTTACCTTTGATGTTTGTAACCCATCTTGGTATCGCTGGATCAACAAC  
CGCCTTGTTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCATGTTTGGTGTAAGAGT  
GATTATAACTGGGGATGCATTTGTTCTGGAGAAAGAAGTGTCAATTATCATGAACCATCGGACAA  
GAATGGACTGGATGTTCTGTGGAATTGCCTGATGCGATATAGCTACCTCAGATTGGAGAAAATT  
TGCCTCAAAGCGAGTCTCAAAGGTGTTCTGGATTTGGTTGGGCCATGCAGGCTGCTGCCTATAT  
CTTCATTCATAGGAAATGGAAGGATGACAAGAGCCATTTGAAGACATGATTGATTACTTTTGTG  
ATATTCACGAACCACTTCAACTCCTCATATCCCAGAAGGGACTGATCTCACAGAAAACAGCAAG  
TCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTCAGAAATATGAATATGTTTTACATCCAAG  
AACTACAGGCTTTACTTTTGTGGTAGACCGTCTAAGAGAAGGTAAGAACCTTGATGCTGTCCATG  
ATATCACTGTGGCGTATCCTCACAACATTCTCAATCAGAGAAGCACCTCCTCCAAGGAGACTTT  
CCCAGGGAAATCCACTTTCACGTCCACCGGTATCCAATAGACACCTCCCCACATCCAAGGAGGA  
CCTTCAACTCTGGTGCCACAAACGGTGGGAAGAGAAAGAAGAGAGGCTGCGTTCCTTCTATCAAG  
GGGAGAAGAATTTTTATTTTACCGGACAGAGTGTCAATCCACCTTGCAAGTCTGAACTCAGGGTC  
CTTGTGGTCAAATTGCTCTCTATACTGTATTGGACCCTGTTTCAGCCCTGCAATGTGCCTACTCAT  
ATATTTGTACAGTCTTGTTAAGTGGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGA  
GAATATTTGGTGGACTGGAGATCATAGAACTGTCATGTTACCGACTTTTACACAAACAGCCACAT  
TTAAATTCAAAGAAAAATGAGTAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTG  
GAAATGTTCTAAACCTTCTAAGCTCAGATGCATTTTTCATGACTATGTCGAATATTTCTTACT  
GCCATCATTATTTGTTAAAGATATTTGCACTTAATTTTGTGGGAAAAATATTGCTACAATTTTT  
TTAATCTCTGAATGTAATTTGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTT  
GGGCCAGAATATTATTAAACAATCATCAGGCTTTTAAA

## **FIGURE 102**

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSGIMVSWKGIYFILTLFWGSFFGSI FMLS P  
FLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVITGDADFVPGERSVIIMNHRTRMDWM  
FLWNCIMRYSYLRLKICLKASLKGVPFGWAMQAAAYIFIHRKWKDDKSHFEDMIDYFCDIHEP  
LQLLIFPEGTDLTENSKSRSNFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLDAVHDITVA  
YPHNIPQSEKHL LQGDFPREIHFHVHRYPIDTLPTSKEDLQLWCHKRWEEKEERLRSFYQGEKNF  
YFTGQSVIPPCKSELRVLVVKLLSILYWTLSFAMCLLIYLSLVKWYFIITIVIFVLQERIFGG  
LEIIEIACYRLLHKQPHLNSKKNE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 44-63, 90-108, 354-377

## FIGURE 103

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGACC  
TCCAAATCATCCATCCACCCCTGCTGTCTATCTGTTTTCATAGTGTGAGATCAACCCACAGGAATA  
TCCATGGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTGGCAAGT  
CACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCCTGCTCCCTCT  
TTCCTGAGACAGTGCAGAGGCTATGGAAGTGCAGTTCTTTCAGGAATCAGTTCCATGCTGTGGTC  
CACCTCTACAGAGATGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCGAGGGAGAACTGA  
GTTTGTGAAGGACTCCATTGTCAGGGGGCGTGTCTCTCTAAGGCTAAAAACATCACTCCCTCGG  
ACATCGGCTGTATGGGTGCTGGTTTCAGTTCCCAGATTACGATGAGGAGGCCACCTGGGAGCTG  
CGGGTGGCAGCACTGGGCTCACTTCTCTCATTTCCATCGTGGGATATGTTGACGGAGGTATCCA  
GTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGCCACAGCCAAGTGGAAAGTCCACAAGGAC  
AGGATTTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAGCCTGTATGATGTGGAGATCTCC  
ATTATAGTCCAGGAAATGCTGGGAGCATATTGTGTCCATCCACCTTGCTGAGCAGAGTCATGA  
GGTGGAAATCCAAGGTATTGATAGGAGAGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTA  
TTTTACTCGGGTTACTCTGTGGTGCCTGTGTGGTTGTTCATGGGGATGATAATTGTTTTCTTC  
AAATCCAAAGGGAATCCAGGCGGAATGGACTGGAGAAGAAAGCACGGACAGGCAGAAATTGAG  
AGACGCCCGAAACACGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCG  
TTTCTGATCTGAAAATGTAACCCATAGAAAAGTCCCCAGGAGGTGCCTCACTCTGAGAAGAGA  
TTTACAAGGAAGAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGA  
CGTGGGACAAAATGTAGGGTGGTATGTGGGAGTGTGCGGGATGACGTAGACAGGGGGAAGAACA  
ATGTGACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTC  
ACATTCAATCCCCATTTTATCAGCCTCCCCCCCCAGCACCCCTCTACACGAGTAGGGGTCTTCCT  
GGACTATGAGGGTGGGACCATCTCCTTCTCAATACAAATGACCAGTCCCTTATTTATACCCTGC  
TGACATGTGAGTTTGAAGCTTGTGAGACCTTATATCCAGCATGCGATGTATGACGAGGAAAAG  
GGGACTCCCATATTTCATATGTCCAGTGTCTGGGGATGAGACAGAGAAGACCCCTGCTTAAAGGGC  
CCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGCCCCAGCTTCCTCT  
CCGGAGCCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCC  
TGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGATTGGCCTGACCCTGTGGGAG  
TCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAA  
CTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCCAGGCTCCTCATTGCTAGTCACGG  
ACAGTGATTCCTGCCTCACAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGCAGGTT  
TGAGGGCACAGTGTGCTAATGATGTGTTTTTATATTATACATTTTCCCACCATAAACTCTGTT  
TGCTTATTCACATTAATTTACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACACC  
TGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTTCTGATTCTATAAGCCCAGCAT  
TACCTGATACCAAAACCAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCC  
CTCATTAAACACAGACACAAAAATTTAAATAAAATTTTAAACAAATTAACTAAACAATATATTTA  
AAGATGATATATAACTACTCAGTGTGGTTTGTCCCAAAATGCAGAGTTGGTTTAAATATTTAAAT  
ATCAACCAGTGAATTGAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAAAAAAAAAAAA

## **FIGURE 104**

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAVVH  
LYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR  
VAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGYSLYDVEISI  
IVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILGLLCGALCGVVMGMIIVFFK  
SKGKIQAELDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAPEVPHSEKRF  
TRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLSPNNGYWVLRLTTEHLYFT  
FNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLTLCQFEGLLRPYIQHAMYDEEKG  
TPIFICPVSWG

### **Signal peptide:**

amino acids 1-17

### **Transmembrane domains:**

amino acids 131-150, 235-259

## FIGURE 105

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAGGAAAAGAG  
TTTGTGGGAACCCCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTCTGGCAGTGTGCATTGGA  
CTCACTGTTTCATTATGTGAGATATAATCAAAGAAGACCTACAATTACTATAGCACATTGTTCATTTACAAC  
TGACAAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAACAATTTTACAGAAATGAGCCAGAGACTTGAAT  
CAATGGTGAAAAATGCATTTTATAAATCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTC  
AGTCAACAGAAGCATGGAGTGTGGCTCATATGCTGTTGATTGTAGATTTCACTCTACTGAGGATCCTGA  
AAGTGTAGATAAAATTTGTTCAACTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAG  
ATCCTCACTCAGTTAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCCGA  
ACACGAAGAAGTAAACTCTAGGTGAGAGTCTCAGGATCGTTGGTGGGACAGAAAGTAGAAGAGGGTGAATG  
GCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCACTCGCTGTGGAGCAACCTTAATTAATGCCACATGGC  
TTGTGAGTGTCTCACTGTTTTACAACATATAAGAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACA  
ATAAAACCTTCGAAATGAAACGGGGTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACA  
TGACTATGATATTTCTCTTGACAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCT  
TCCCTGATGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAAAT  
GATGGTTACAGTCAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACTTGCAATGAACC  
TCAAGCTTACAATGACGCCATAACTCCTAGAAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGCAT  
GCCAGGGTGACTCTGGAGGACCACTGGTTAGTTTCAGATGCTAGAGATATCTGGTACCTTGCTGGAATAGTG  
AGCTGGGGAGATGAATGTGCGAAACCAACAAGCCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTG  
GATTACTTCAAAAACTGGTATCTAAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTGT  
GGTGTGGAGGCCATTTTATAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCA  
ATAAACTGTTTGCTTGATGCATGATTTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCA  
GATCAACTCTGTCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATAATACAATATTAC  
ATTACAGCCTGTATTCATTTGTTCTCTAGAAGTTTGTGTCAGAAATTTGACTTGTGACATAAATTTGTAAT  
GCATATATACAATTTGAAGCACTCCTTTCTTCAGTTCCTCAGCTCCTCTCATTTCAGCAAATATCCATTT  
TCAAGGTGCAGAACAAGGAGTGAAAGAAAATATAAGAAGAAAAAATCCCCTACATTTTATTGGCACAGAA  
AAGTATTAGGTGTTTTCTTAGTGGAATATTAGAAATGATCATATTTCATTATGAAAGGTCAAGCAAAGACA  
GCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAAGTAAAGTAAAGGAAGTCCAGAAAGAAGCCAAG  
ATATATCCTTATTTTCATTTCCAAACAACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTGTGACCT  
ATAATAATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATATTTATTTAACATTG  
TTACTGAGGATGTCAACATATAACAATAAATATAAATCACCCA

## **FIGURE 106**

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTNYYSTLSFTTDKLY  
AEFGREASNNFTEMSQRLESMVKNAFYKSPLEEFVKSQVIKFSQQKHGVLAHMLLICRFHSTED  
PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG  
TEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIKPSKMKRGL  
RRIIVHEKYKHPSHDYDISLAELSSPVYTNVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS  
QNHRLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSSGGLVSSDARDIWYLAG  
IVSWGDECAKPNKPGVYTRVTALRDWITSKGTGI

**Transmembrane domain:**

amino acids 21-40 (type II)

## FIGURE 107

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCCTG  
 CCCCAGATGAGCCCCCGCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCGGGCCAGC  
 GCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTCTCCCTT  
 ACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTCTACGCCCTCAA  
 TCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGGGACTACCTAA  
 ATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTTACTTTCCT  
 GTGGTTCATCCGGTCATGATTGCTGTTGCTGTTTCCTTATCATTGTGGGGATGTTAGGATATTG  
 TGAACGGTGAAAAGAAATCTGTTGCTTCTTGCAATGTTGAAAGTTTGTGCTATTCTTCT  
 GTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACCTATGGTTCCAGTACAATGGTCA  
 GATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCCGTGGCTTACTCA  
 TGCTTGGAAATTTTTTTCAGAGAGAGTTAAGTGTGTGGAGTAGTATATTTCACTGACTGGTTGG  
 AAATGACAGAGATGGACTGGCCCCCAGATTCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA  
 CAGGCCACCAAGAGATCTCAGTGACCTTTATCAAGAGGGTGTGGGAAGAAAATGTATTCCTT  
 TTTGAGAGGAACCAACAACAGTGCAGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAA  
 TCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCTGGG  
 ACAGACCAAATGATGTCCTTGAAGAATGACAACCTCTCAGCACCTGTCATGTCCCTCAGTAGAACT  
 GTTGAAACCAAGCCTGTCAAGAATCTTGAACACACATCCATGGCAAACAGCTTTAATACACACT  
 TTGAGATGGAGGAGTTATAAAAAGAAATGTCACAGAAGAAAACCACAAACTTGTTTTATTGGACT  
 TGTGAATTTTGTAGTACATACTATGTGTTTTCAGAAATATGTAGAAATAAAATGTTGCCATAAAA  
 TAACACCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTC  
 ACCACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCC  
 TGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCGCA  
 TCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTACTTCTACCAA  
 CTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA  
 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACCTTCAATATTGGTGACT  
 ACCTAAATGTGATTTTTGCTGGTTACTAAATATCTTACCCTTAAAGAGCAAGCTAACACAT  
 TGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCAGTCGAT  
 TTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCTGTATAGCATCATT  
 ATTTTGTAGCCTTTCTGTTAATAAAGCTTTACTATTCTGTCTGGGCTTATATTACACATATAAC  
 TGTATTTTAAATACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTC  
 AGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTTCAGA  
 AAGGACTTGTATGCTGTTTTCTCCCAAATGAAGACTCTTTTGGACACTAAACACTTTTTAAAAA  
 GCTTATCTTTGCCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAA  
 TAGTGTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAACATGTGACAATTTAGAGATT  
 CTTTGTATTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTTTTACAA  
 GAGTATAGTATATTTATTTGAAATGGGAAAAGTGCAATTTTACTGTATTTTGTGATTTTGTATT  
 TTCTCAGAAATATGGAAGAAAATTTAAATGTGTCAATAATATTTTCTAGAGAGTAA

## **FIGURE 108**

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPVVHP  
VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVT  
LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREFPGCSKQAHQ  
EDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDRREPSTDQM  
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

### **Signal peptide:**

amino acids 1-33

### **Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248



## FIGURE 109

CCAAGGCCAGAGCTGTGGACACCTTATCCCACCTCATCCTCATCCTCTTCTCTGATAAAGCCCCCTACCAGTGCT  
GATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCTTAAAAAAAAGTGCTTGAAGAGAAGGGGACAAAGGAACA  
CCAGTATTAAGAGGATTTTCCAGTGTTTCTGGCAGTTGGTCCAGAAGGATGCTCCATTCTGCTTCTCACCTG  
CCTCTTCATCACAGGCACCTCCGTGTCACCCGTGGCCCTAGATCCTTGTCTGCTTACATCAGCCTGAATGAGC  
CCTGGAGGAACACTGACCACCACTGGATGAGTCTCAAGGTCTCTCTATGTGACAACCATGTGAATGGGGAG  
TGGTACCACCTTACGGGGCATGGCGGGAGATGCCATGCCTACCTTCTGCATACCAGAAAACCACTGTGGAACCCA  
CGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAGGCGACGGCATTGTGCAACGCCAGGCTTGTGCCAGCT  
TCAATGGGAACCTGCTGTCTCTGGAACACCACGGTGAAGTCAAGGCTTGCCCTGGAGGCTACTATGTGTATCGT  
CTGACCAAGCCCAGCGTCTGCTTCCACGTCTACTGTGGTCATTTTATGACATCTGCGACGAGGACTGCCATGG  
CAGCTGCTCAGATACCAGCGAGTGCACATGCCTCCAGGAAGTGTGCTAGGCCCTGACAGGCAGACATGCTTTG  
ATGAAATGAATGTGAGCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTCCTACCGTGT  
GAGTGTGGGGTTGGCCGTGTGCTAAGAAGTGTGGAAGACTTGTGAAGACGTTGAAGGATGCCACAATAACAA  
TGGTGGCTGCAGCCACTTGTGCTTGGATCTGAGAAAGGCTACCAGTGTGAATGTCCCCGGGGCCTGGTGTGT  
CTGAGGATAACCACACTTGCCAAAGTCCCTGTGTTGTGCAAAATCAAATGCCATTGAAAGTGAACATCCCCAGGGAG  
CTGTTTGGTGGCCCTGGAGCTCTTCTGACCAACACCTCCTGCCGAGGAGTGTCCAACGGCACCCATGTCAACAT  
CCTCTTCTCTCTCAAGACATGTGGTACAGTGGTTCGATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGA  
CAGGTCTACCCAAGCAGACCCCGGGGAGCAGCGGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCGGTG  
ACCTGCGAGTTTCCACGCCTGTACACCATTTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCCACTGGAAT  
CATGAGCCGAAATCATGGGATCTTCCATTCACTCTGGAGATCTTCAAGGACAATGAGTTTGAAGAGCCTTACC  
GGGAAGCTCTGCCCCACCTCAAGCTTCGTGACTCCCTCTACTTTGGCATTGAGCCCCTGGTGCACGTGAGCGGC  
TTGGAAGCTTGGTGGAGAGCTGCTTTGCCACCCACCTCCAAGATCGACGAGTCTGAAATACTACCTCAT  
CCGGGATGGCTGTGTTTCAGATGACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCCAGG  
TCCCTGTCTTCAAGTTTGTGGGCAAAGACCACAAGGAAGTGTTCCTGCACTGCCGGGTTCTTGTCTGTGGAGTG  
TTGGACGAGCGTTCCCGCTGTGCCAGGGTTGCCACCGGCAATGCGTCTGGGGCAGGAGGAGAGGACTCAGC  
CGGTCTACAGGGCCAGACGCTAACAGGCGGCGCGATCCGCATCGACTGGGAGGACTAGTTCGTAGCCATACCTC  
GAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTCCCCCACCAGCCCTTAAGAATCTGCCAACAGC  
TGGGTTCAAGACTTCACTGTGAGTTCAGACTCCCAGCACCACTCACTCTGATTCTGGTCCATTCACTGGGCA  
CAGGTCACAGCACTGCTGAACAATGTGGCCTGGGTGGGGTTTCATCTTTCTAGGGTTGAAAACCTAACTGTCCA  
CCCAGAAAGACACTCACCCCATTTCCCTCATTTCTTCTTACACTTAAATACCTCGTGTATGGTGAATCAGAC  
CACAAAATCAGAAGCTGGGTATAATATTTCAAGTTACAACCCCTAGAAAAATTAACAGTTACTGAAATTATGA  
CTTAAATACCCAATGACTCCTTAAATATGTAAATTATAGTTATACCTTGAAATTTCAATTCAAATGCAGACTAA  
TTATAGGGAATTTGGAAGTGATCAATAAACAGTATATAATTTT

## **FIGURE 110**

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHLQDESQGPFLCDNHVNGEWYHFTGMAGDAMP  
TFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASENGNCCLWNTTVEVKACPGGYVYRLTKPSVCFHV  
YCGHFYDICDEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV  
LRSDGKTCEDEVEGCHNNNGGCSHSLGSEKGYQCECPRGLVLSNHTCQVPVLCKSNAIEVNIIPRELVGG  
LELFLTNTSCRGVSNTHVNLFLSLKTCGTVVDVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT  
CEFPRLYTISEGYVPNLRNSPLEIMSRNHGIFPFTLEIFKDNEFEPPYREALPTLKLRLDSLYFGIEPVVHV  
SGLESLVESCFATPTSKIDEVLKYILIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRV  
LVCGVLDERSRCAQGGCHRRMRGAGGEDSAGLQGQTLTGGPRIIDWED

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-16

#### **N-glycosylation sites.**

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

#### **Tyrosine kinase phosphorylation sites.**

amino acids 411-418, 443-451

#### **N-myristoylation sites.**

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,  
522-528, 531-537

#### **Aspartic acid and asparagine hydroxylation site.**

amino acids 197-209

#### **ZP domain proteins.**

amino acids 431-457

#### **Calcium-binding EGF-like proteins.**

amino acids 191-212, 232-253

## FIGURE 111

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGG  
GCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCT  
CCTGCTGCCCTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGT  
TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCC  
ATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGT  
GGTTGTCTCATCAAGGTGATTCTGGATAAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCGA  
GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC  
CCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCAC  
AGGGAAGTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATGG  
GCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGATGTTGTTGAAATCACAGAAACAGCCAG  
GAGCTTCGCATGCGGAACCTCAAGTGGGCCCTGTCTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCTG  
TGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGG  
TCAGCATCCAGTACGACAAACAGCAGCTGTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCA  
GCCCCTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGCAG  
CTTCCCCTCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAAAGACAATGACA  
TCGCCCTCATGAAGCTGCAGTTCCTCACTTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTT  
GATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAA  
GATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCAATTGACAGCACACGGTGCAATGCAGACGATGCGT  
ACCAGGGGGAAAGTCAACGAGAAGATGATGTGTGCAGGCATCCCGAAGGGGGTGTGGACACCTGCCAGGGT  
GACAGTGGTGGGCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGG  
CTGCGGGGGCCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCT  
GGAAGGCTGAGCTGTAATGCTGCTGCCCCTTTGACGTGCTGGGAGCCGCTTCCTTCCTGCCCTGCCACCT  
GGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCTTGGGTACACCCCTCTGCCACAGCCTCAGCAT  
TTCTTGGAGCAGCAAAGGGCCTCAATTCTGTAAAGAGACCCTCGCAGCCAGAGGCGCCAGAGGAAGTCA  
GCAGCCCTAGCTCGGCCACACTTGGTGCTCCAGCATCCAGGGAGAGACACAGCCCACTGAACAAGGTCT  
CAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAAGCC  
CAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTCACCCATCCCCAA  
GCCTACTAGAGCAAGAAACAGTTGTAATATAAAATGCACGTGCCCTACTGTTGGTATGACTACCGTTACCT  
ACTGTTGTCATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAA  
AAAA

## **FIGURE 112**

MLQDPDSQPLNSLDVKPLRKPRIPMETFRKVGIPIIIIALLSLASIIIVVLIKVILDKYYFLCG  
QPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAAVAVRLSKDRSTLQVLDSATGNWFSACFDN  
FTEALAEACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNSSGPCLSGSLVSLHCLACGKSL  
KTPRVVGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWLTAAHCFRKHTDVFNWKVRAGSDKL  
GSFPSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWG  
FTKQNGGKMSDILLOASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCCQDSSGGPLMYQS  
DQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

**Transmembrane domain:**

amino acids 32-53 (typeII)

## FIGURE 113

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCTCAGCCTCCCAAGGTGCTGTGATTA  
TAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTTCAGCAACTAAAAAGCCACAGGAGT  
TGAACCTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATTAAAAATC  
TGTTTTTTGTTCTCTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGTCACTGTGGCTCT  
GGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGTCCCCCTCGAAG  
CCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCACCTGTCTCACGTCT  
GGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGCTAGCTGCGGCTTTCAAGGTGGGC  
CTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCGAAGATTTTCATAGGCGATGGCTCCCCTGCCC  
AGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGGGCGTGGACACCTGCTCA  
GAAGCAGTGGGTGAGACATCACGCTGCCCGCCCATCTAACCTTTTCATGTCTGCACATCACCTG  
ATCCATGGGCTAATCTGAACCTCTGTCCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC  
CAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGACTTGCACTTCTCCTGGAACATGAGG  
GAACGCCGAGGAAAGCAAAGTGGCAGGGAAGGAACCTGTGCCAAATTATGGGTGAGAAAAGATG  
GAGGTGTGGGTTATCACAAGGCATCGAGTCTCCTGCATTCACTGGACATGTGGGGGAAGGGCTG  
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGAT  
CCACGTACCAGCTGCTGAAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAA  
TCTGCGATCACCAGCCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCC  
CTCCTTCCCTCTGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG  
GGCTAATGGCTCAGTGTGGCCAGGAGGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCT  
GTGCGAACACGGAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGG  
CTCAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCAAGACCAAAGGAGCTAGAGCTTGTT  
CAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAAATCCA  
AACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACAT  
TTTGGGAGGCCGAGGCGGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGG  
TGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATC  
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACA  
GGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAAGAATTA  
TGGTTATTTGTAA

## **FIGURE 114**

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTASPC  
WPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

**Signal peptide:**

amino acids 1-15

10063534

## FIGURE 115

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGCAA  
AGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAA  
ATATGTAAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCTAATTGTCCT  
GTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGAGCACACTT  
TCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAGAACTGAAATA  
TTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAACGGATACACTGG  
CATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAAACTCAGATTAAAGTGATTCTGAATTTT  
CTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACCTTTCTTTGAACAGTCAGTG  
ATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAAAAATTCCAAAATTCTGGA  
GATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAG  
ACTTTGAGGAGGAGGAGAGAAGATCTTCACTTTCTGCCAACGAAAAAAAGGGATTGAACAAAAT  
GAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCGTACGCCAGACAAGCAAGTGAGGA  
AGAACTTCCAATAAATGACTATACTGAAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAG  
GTTATTGTTGTATTTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTA  
GGCTACTACCCATATCCATACTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTG  
TAACTGGTGGGTGGCCCGCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAAAC  
TGCTGGCAACATATAATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCT  
GGTAGCCAGCTCTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACA  
TTATCACCAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 116**

MAKNPPENCEDCHILNAEAFKSKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAYDME  
HTFYNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTG IYFVGLQKCFIKTQIKVIP  
EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKN SKILEICDNVTMYWINPTLISVSE  
LQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLD  
ERGYCCICYRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14



## FIGURE 117

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGCAGGCGGCA  
GGGCGGGCGGCCAGGATCATGTCCACCACCACATGCCAAGTGGTGGCGTTCCTCCTGTCCATCCTGGGGCT  
GGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGACCCAGGACCTGTACGACAACCCCGTCACCT  
CCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCC  
TATTCACCATCCTGGGACTTCCAGCCATGCTGCAGGCAGTGCGAGCCCTGATGATCGTAGGCATCGTCCT  
GGGTGCCATTGGCCTCCTGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG  
CCAAAGCCAACATGACACTGACCTCCGGGATCATGTTTATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTG  
TCTGTGTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTGG  
GATGGTGCAGACTGTTTACAGCCAGGTACACATTTGGTGCGGCTCTGTTCTGGGGCTGGGTGCTGGAGGCC  
TCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCCTGGCACCAGAAGAAACCACTACAAA  
GCCGTTTCTTATCATGCCTCAGGCCACAGTGTGCTTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTT  
TGGGTCCAACACCAAAAACAAGAAGATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATC  
CTTCCAAGCAGACTATGTGTAATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCA  
CCCCAAAAACAAGGAGATCCCATCTAGATTTCTTCTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGCCT  
CGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCATAAAACA  
GCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTTCTTTTTTAAATATAACT  
TTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTTAGACAGACTCCCCCTC  
TTCTCTCTAGTCAATAAACCATTGATGATCTATTTCCAGCTTATCCCCAAGAAAACTTTTGAAAGGAAA  
GAGTAGACCCAAAGATGTTATTTTCTGCTGTTTGAATTTGTCTCCCCACCCCCAACTTGGCTAGTAATAA  
ACACTTACTGAAGAAGAAGCAATAAGAGAAAAGATATTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTT  
ACACTGTGATCTTAAAAGTTACCAACCAAGTCATTTTCAGTTTGAGGCAACCAACCTTTCTACTGCTG  
TTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAGTCTCTTTCTGT  
CGCGGGTCAGAAATGTCCCTAGATGAATGAGAAAATTATTTTTTTAATTTAAGTCCTAAATATAGTTAA  
AATAAATAATGTTTTAGTAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAGAAG  
GAAATGAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCC  
ATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGT  
TCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCA  
TGGTGGCATAACCTGTAGTCCCAGCATTCGGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGT  
TGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAA  
AATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAACTAATTCTTTAA

## **FIGURE 118**

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTECRP  
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSI FALKCIRIGSMEDSAKANMTLTSGIMFIVSGL  
CAIAGVSVFANMLVTNEFMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA  
CRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYPSKHDY  
V

### **Signal peptide:**

amino acids 1-23

### **Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

APP ID=10063534

## FIGURE 119

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGGAGTCC  
 AGCTGGCTAAAACATCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTG  
 GTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGGAGAGTGTCCGCCTTCATT  
 GAAAAACAACATCGTGGTTTTTGAAGCTTCTGGGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA  
 CATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTTCTCCGGACCTACAGGCAGCCAGAG  
 GACTGATGTGTGCTGCTTCCGTGATGTCCTTCTGGCTTTCATGATGGCCATCCTTGGCATGAAATGC  
 ACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCAT  
 CATCAGGGCATGGTGGTGTCTATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATA  
 ACTCAATAGTGAATGTTGCCCAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCA  
 CTGGTGTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTGTGCAACGAAAAGAGCAGTAGCTA  
 CAGATACTCGATACCTTCCCATCGCACAAACCAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCG  
 TCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTAACTTTACTATAAGCCATGCAAAATG  
 ACAAAAATCTATATTACTTTCTCAAAATGGACCCCAAGAACTTTGATTTACTGTTCTTAACTGCCT  
 AATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATTTACGAGAATGAGATA  
 TTAAACCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGGTTCAGCATCTA  
 CTCTTTTATCATTTACTTCAAAATGACATTGCTAAAGACTGCATTATTTTACTACTGTAATTTCTCC  
 ACGACATAGCATTATGTACATAGATGAGTGTAAACATTTATATCTCACATAGAGACATGCTTATATGGT  
 TTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAA  
 ATCATGGATAGGGTTGAAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCA  
 TTTATAATGAAGATTAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATAT  
 GCTGTTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTTT  
 CTTGTGTATTAAATTAACATTTTTTAAACGCAGATATTTTGTCAAGGGGCTTTGCATTCAAACGCTT  
 TTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTG  
 AAAATATTTTTGTTTTGTATTTGAAGAAGAATGATGCATTTTGACAAGAAATCATATATGTATGGAT  
 ATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAGAGCAGAAAAATA  
 TGTCTTGGTTTTTCAATTTGCTTACCAAAAAACAACAACAAAAAAGTTGTCTTTGAGAACTTCACCT  
 GCTCCTATGTGGGTACCTGAGTCAAAATGTCAATTTTTGTTCTGTGAAAAATAAATTTCTTCTTGT  
 CCATTTCTGTTTAGTTTTACTAAAATCTGTAAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAA  
 ACTGACAATCCAATTTGAAAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTGCTT  
 TATACATTTATATTAATAAATGTACATTTTTCTAATT

## **FIGURE 120**

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRMQCK  
IYDSSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGIIFIITG  
MVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCNEKSSSY  
RYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

### **Signal peptide:**

amino acids 1-17

### **Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

## FIGURE 121

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAG  
CCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCCTCCAGCTCCGCGCTGCCCGGCAGCC  
GGGAGCCATGCGACCCAGGGCCCCGCGCCTCCCCGAGCGGCTCCGCGGCCTCCTGCTGCTCC  
TGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAGGCGCAG  
CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC  
TGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCCCAGGTCGGGATG  
GATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAGCTTTGAGGAGTCTTGACACCCAACTAC  
AAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGACATT  
TACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTGTTCAGTGGCTCACTTCGGCTAAAATGCA  
GAAATGCATGCTGTCAGCGTTGGTATTTACATTCAATGGAGCTGAATGTTTCAGGACCTCTTCCC  
ATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCG  
CACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG  
TTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATC  
ATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCC  
TTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAG  
CTAAATATGTTTACAGACCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCAATTTG  
CTTCAATCAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATT  
CTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTA  
AAAAAATATAAAGCTACCAATCTTTGTACAATTGTAAATGTTAAGAATTTTTTTTATATCTGT  
TAAATAAAAATTATTTCCAACA

## **FIGURE 122**

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAQVPGR  
DGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTK  
MRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIYLDQGSPEMNSTINIHRTS  
SVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK

### **Signal peptide:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 195-217

## FIGURE 123

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTGAA  
 CTGGGTGCTCATCAGGGAAGTCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA  
 ATTGCCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATGTAGGATCCAGTTTTTTTTTTA  
 ACCGCCCCCTCCCCACCCCCAAAAAACTGTAAAGATGCAAAAACGTAATATCCATGAAGATCC  
 TATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATTTATTTGTTCTTGGAG  
 TGTTCGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAGGGGTCCAATTTT  
 TCTTCCTGGGTGTGAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGGTGTGATGCAACTG  
 GCCCCAAGCCAAAGCAAAGACCTAAGGACGACCTTTGAACAATACAAAGGATGGGTTTCAATG  
 TAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCACTGTCTTACTGACAATG  
 CTTTCTTCTGCGAAGCAGGATGCCCTAAGGGCTGTAGGTGTGAAGGCAAAATGGTATATTGTGA  
 ATCTCAGAAATTACAGGAGATACCCCTCAAGTATATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCT  
 ATAACAGCCTTCAAAACTTAAGTATAATCAATTTAAAGGGCTCAACCAGCTCACCTGGCTATAC  
 CTTGACCATAACCATTCAGCAATATTGACGAAAATGCTTTTAAATGGAATACGAGCTCAAAGA  
 GCTGATTCTTAGTTCCAAATAGAATCTCCTATTTTCTTAAACAATACCTTCAGACCTGTGACAAAT  
 TACGGAAGCTTGGATCTGTCTATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTG  
 CGGAAGCTGCTGAGTTTACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCA  
 AGACTGCCGCAACCTGGAAGCTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATG  
 TCTTTGCTGGCATGATCAGACTCAAAGAACTTCACTGGAGCACAATCAATTTTCCAAGCTCAAC  
 CTGGCCCTTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGAATAAAATCAGTGT  
 CATAGGACAGACCATGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGA  
 TCGAAGCTTTCAGTGGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGAT  
 TCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACATCAG  
 TCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAAGCTGGCTGAAAAGTT  
 TTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAAATGTG  
 ATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGATCTGGCCAG  
 GGCTCTCCCAAAGCCGACGTTTAAAGCCCAAGCTCCCCAGGCCGAAGCATGAGAGCAAACCCCTT  
 TGCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGCTGACGCCGAGCACATCTCT  
 TTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCGTGCTCGTCATCCTGCTGGTTAT  
 CTACGTGTCATGGAAGCGGTACCCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAA  
 GGCACAGGAAAAAGAAAGACAGTCCCTAAAGCAAATGACTCCAGCACCCAGGAATTTTATGTA  
 GATTATAAACCCACCAACACGGAGACCAGCGAGATGCTGCTGAATGGGACGGGACCCTGCACCTA  
 TAACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACCATTGTGATAAAAAGAGCTCTTAAAGCT  
 GGGAAATAAGTGGTGTCTTATTGAACTCTGGTGACTATCAAGGGAACGCGATGCCCCCTCCCC  
 TTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCCCTGTCCGTTTTAGTGCATTCTAATACT  
 GGTCAATTTTCTCTCATACATAATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTT  
 GAACTCCGGTTTAAATATAATACCTATTGTATAAGACCCTTTACTGATTCCATTAATGTGCAATTT  
 GTTTTAAGATAAACTTCTTTCATAGGTAAAAA

## **FIGURE 124**

MGFNVIRLLSGSAVALVIAPTIVLLTMLSSAERGCPKGCRCGKMVYCESQKLQEIPSSISAGCLG  
LSLRYNLSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYFLNNTFR  
PVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIFQDCRNLELLDLGYNRIRS  
LARNVFAGMIRLKEHLHLEHNQFSKLNALFPRLVSLQONLYLQWNKISVIGQTMSWTWSSLQRLDL  
SGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIGQEILDSWISLNDISLAGNIWECSRNICSLVN  
WLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKPTFKPKLPRPKHE  
SKPPLPPTVGATEPGPETDADAHEHISFHKIIAGSVALFLSVLVILLVIYVSWKRYPASMKQLQQR  
SLMRRHRKKKRQSLKQMTPTSTQEFYVDYKPTNTETSEMLLNGTGPCTYNKSGSRECEV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-33

#### **Transmembrane domain:**

amino acids 420-442

#### **N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

#### **Tyrosine kinase phosphorylation site.**

amino acids 136-142

#### **N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512



## FIGURE 125

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCGCTG  
ACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGCCGAGCT  
AGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAGCTCTTGCTC  
GGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACAGCCCTAGGGATC  
ATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCATTTACAGACACGTAGT  
GTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTTGGCAAAAGTGAAG  
ATGAGCATTATCCCCCTTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTGGCCAGTTT  
TTAGCCAATCCAACCTGACCTAGTGAAGGTTGAGATGCAAATGGAAGGAAAAAGGAACTGGAAGG  
AAAACCATTCGATTTCGTGGTGTACATCATGCATTTGCAAAAATCTTAGCTGAAGGAGGAATAC  
GAGGGCTTTGGGCAGGCTGGGTACCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTA  
ACCACCTATGATACAGTGAAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGAC  
TCACGGTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCA  
TCAAAGCAGAATAATGAATCAACCACGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCG  
ACTGACTGCTTGATTCAAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACC  
ATCTTGGCTGAGAAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAATCAGAGAGA  
TGAGTGGAGTCAGTCCATTTTAA

## **FIGURE 126**

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGARES  
APYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVGKSEDEHYPLWKS  
VIGGMMAGVIGQFLANPTDLVKVQMOMEGKRKLEGKPLRFRGVHHAFAKILAEGGIRGLWAGWVP  
NIQRAALVNMGDLTTYDTPVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTPADVIKSRIMNQP  
RDKQGRGLLYKSSTDCLIQAVQGEFMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

### **Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

## FIGURE 127

CGCGGATCGGACCCAAGCAGGTCGGCGGCGGGCAGGAGAGCGGCCGGGCGTCAGCTCCTCGAC  
CCCCGTGTCGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCCATGGCCAGGCCCGGCATGG  
AGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCTCGGGGGGCATCGGCGCGGCCGTGGCC  
CGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAACATCGAGGA  
GCTGGCTGCTGAATGTAAGAGTGACAGGCTACCCCGGGACTTTGATCCCCTACAGATGTGACCTAT  
CAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATC  
TGCATCAACAATGCTGGCTTGGCCCCGCTGACACCCTGCTCTCAGGCAGCACCACTGGTTGGAA  
GGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCAGTCCATGA  
AGGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTTA  
CCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCACCTGCGCTGACAGAGGGACT  
GAGGCAAGAGCTTCGGGAGGCCCAGACCCACATCCGAGCCACGTGCATCTCTCCAGGTGTGGTGG  
AGACACAATTGCGCTTCAAACCTCCACGACAAGGACCCTGAGAAGGCAGCTGCCACCTATGAGCAA  
ATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTTATCTACGTCTCAGCACCCCGCACA  
CATCCAGATTGGAGACATCCAGATGAGGCCCACGGAGCAGGTGACCTAGTGACTGTGGGAGCTCC  
TCCTTCCCTCCCCACCCTTCATGGCTTGCCTCCTGCCTCTGGATTTTAGGTGTTGATTTCTGGAT  
CACGGGATACCACTTCTGTCCACACCCCGACCAGGGGCTAGAAAATTTGTTTGAGATTTTATA  
TCATCTTGTCAAATTGCTTCAGTTGTAAATGTGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCC  
TAATTGTTTTACTTGTAACTTGTCTTGTGCCCTGGGCACCTTGGCCTTTGTCTGCTCTCAGTG  
TCTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAAATCCCCATCTTCTTGACCTCAACGTCTG  
TGGCTCAGGGCTGGGGTGGCAGAGGGAGGCCTTACCTTATATCTGTGTTGTATCCAGGGCTCC  
AGACTTCCTCCTCTGCCTGCCCCACTGCACCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCC  
AGCCCAGTCTTGGCTTCTTGTCCCTCCTGGGTCATCCCTCCACTCTGACTCTGACTATGGCAG  
CAGAACACCAGGGCCTGGCCCAGTGGATTTCATGGTGATCATTAAAAAGAAAAATCGCAACCAA  
AAAAAAAAA

## **FIGURE 128**

MARPGMERWRDRLALVTGASGGIGAAVARALVQQGLKVVGCARTVGNIEELAAECKSAGYPGTLI  
PYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLTLLSGSTSGWKDMFNVNVLALSICTR  
EAYQSMKERNVDDGHIININMSGHRVPLSVTHFYATKYAVTALTEGLRQELREAQTHIRATC  
ISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

Important features of the protein:

Signal peptide:

amino acids 1-17

N-myristoylation sites.

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,  
199-205

Short-chain alcohol dehydrogenase.

amino acids 30-42, 104-114

## FIGURE 129

AACTTCTACATGGGCCTCCTGCTGCTGGTGTCTTCCTCAGCCTCCTGCCGGTGGCCTACACCAT  
CATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTCAAGTGCAGAGTCTCAGTTGCCCGGGAGC  
ACCTCCCCTCCCAGGGCAGTCTGCTCAGAGGGCCTCGGCCCAAGATTCCAGTTCTGGTTTCATGC  
CAGCCTGTAAAAGGCCATGGAACTTGGGTGAATCACCGATGCCATTTAAGAGGGTTTTCTGCCA  
GGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTCAATTTAGTAGCCACCAGCCACCTGTGG  
CCGTTGAGTGCTTGAAATGAGGAAGTGAAGAAATTAATTTCTCATGTATTTTTCTCATTTATTTA  
TTAATTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGGATACATGTATACAA  
TATATAATGATCAAATCAGGGTAAGTGGGATATCCATCACATCAAACATTTATTTTTTATTCTTT  
TTAGACAGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAAC  
CTCTGCCCTGCCAGGTTCAAGCGATTCTCATGCCCTCCACCTCCCAAGTAGCTGGGACTACAGGCAT  
GCACCACAATGCCCACTAATTTTTGTATTTTTAGTAGAGACGGGGTTTTGCCATGTTGCCCAGG  
CTGGCCTTGAACTCCTGGCCTCAAACAATCCACTTGCCCTCGGCCTCCCAAGTGTTATGATTACA  
GGCGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTTCTTTGTGTTGGGAACTTTGAAATTAT  
ACAATGAATTATTGTTAACTGTCACTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCT  
ATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTCATCCCCACTCCTCTCTATCCTTCCC  
AACCTCTGATCACCTCATTCTACTCTCTACCTCCATGAGATCCACTTTTTTAGCTCCCACATGTG  
AGTAAGAAAATGCAATATTTGTCTTTCTGTGCCTGGCTTATTTCACTTAACATAATGACTTCCTG  
TTCCATCCAIGTTGCTGCAAATGACAGGATTTCTGTTCTTAATTTCAATTAAAATAACCACACATG  
GCAAAAA

## **FIGURE 130**

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRIPVLVSCQPV  
KGGHTLGESPMFPKRVCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

## FIGURE 131

TTCTGAAGTAACGGAAGCTACCTTGTATATAAGACCTCAACACTGCTGACCATGATCAGCGCAGCCTGGAGC  
ATCTTCCTCATCGGGACTAAAATTGGGCTGTTCCCTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCTG  
TCCATCTGTGTGCTGCGATGCGGGTTTCATTTACTGTAATGATCGCTTTCTGACATCCATTCCAACAG  
GAATACCAGAGGATGCTACAACCTCTACCTTCAGAACAACCAAATAAATAATGCTGGGATTCCCTTCAGAT  
TTGAAAAACTTGCTGAAAGTAGAAAGAATATACCTATACCACAACAGTTTAGATGAATTTCCACCAACCT  
CCCAAAGTATGTAAGAGTTACATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAA  
AAATTCCCTATCTGGAAGAATTACATTTAGATGACAACCTCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCA  
TTCCGAGACAGCAACTATCTCGACTGCTTTTCCTGTCCCGTAATCACCTTAGCACAATTCCCTGGGGTTT  
GCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTTCATCACCATCTCTTCAAG  
GTCTCACTAGTCTAAACGCTGTTCTAGATGGAACCTGTTGAACAATCATGGTTTAGGTGACAAAGTT  
TTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCGGAATCCCTGACTGCTGCACCAGTAAACCT  
TCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATAACCACATCAATCGGGTGCCCCAAATGCTTTTT  
CTTATCTAAGGCAGCTCTATCGACTGGATATGTCCAATAATAACCTAAGTAATTTACCTCAGGTATCTTT  
GATGATTTGGACAATATAACACAACCTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATG  
GGTACGTGACTGGTTACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAA  
AGGTTTCGTGGGATGGCTATTAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAAGC  
ACCATTGAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCAAGGACAGTGGCCAGCTCCAGTGAC  
CAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAGGGAGTCCCTCAAGAAAAA  
CAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTATCTCTTGGAACCTTGCTCTACCTATG  
ACTGCTTTGAGACTCAGCTGGCTTAAACTGGGCCATAGCCCGGCATTTGGATCTATAACAGAAACAATTGT  
AACAGGGGAACGCAGTGAGTACTTGGTCACAGCCCTGGAGCCTGATTACCCCTATAAAGTATGCATGGTTC  
CCATGGAAACCAGCAACCTCTACCTATTTGATGAAACTCCTGTTTGATTGAGACTGAAACTGCACCCCTT  
CGAATGTACAACCCCTACAACCACCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAACCCCAATTTACC  
TTTGGCTGCCATCATTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTGGTATG  
TTCATAGGAATGGATCGCTCTTCTCAAGGAACGTGCATATAGCAAAGGGAGGAGAAGAAAGGATGACTAT  
GCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAACCTTCTTTTCAGATGTTACCAAT  
AAGCAATGAACCATCTCGAAGGAGGAGTTTGAATACACACCATATTTCCCTCTAATGGAATGAATCTGT  
ACAAAACAATCACAGTGAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCAGACTCAGATCAC  
TCACACTCATGATGCTGAAGGACTCACAGCAGACTTGTGTTTTGGGTTTTTTAAACCTAAGGGAGGTGATG  
GT

## **FIGURE 132**

MISAAWSIFLIGTKIGLEFLQVAPLSVMAKSCPSVCRC DAGFIYCND RFLTSIPTGIPEDATTLYL  
QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIR TITYDSLSKIPYL  
EELHLLDDNSVSAVSIEEGA FRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRISTISSPSL  
QGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKLYLQDNHIN  
RVPPNAFSYLRLQLYRLDMSNNNLSNLPQGIFDDLDNITQLILRN NPWYCGCKMKWVRDWLQSLPV  
KVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQGQWPAPVTKQPD  
IKNPKLTKDQQTGSPSRKTITITVKSVTSDTIHISWKLALPMTALRLSWLKLGHSPAFGSITET  
IVTGERSEYLVTALEPDSPYKVC MVPMETSNLYLFDET PVC IETETAPLRMYNP TTTLNREQEKE  
PYKNPNLPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSKGRRRKDDYAEAGTKKDNS  
ILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNL YKNNHSESSSNRSYRDSGIPDS DHSHS

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 531-552

#### **N-glycosylation sites.**

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

#### **Tyrosine kinase phosphorylation site.**

amino acids 515-522

#### **N-myristoylation sites.**

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,  
640-645

#### **Amidation site.**

amino acids 567-570

#### **Leucine zipper pattern.**

amino acids 159-180

#### **Phospholipase A2 aspartic acid active site.**

amino acids 34-44



## FIGURE 133

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCAGGCCACCCAGGCTTCTTGGA  
GCCCTGCCGGGCCACTTGTCTTCAATGTCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAGGGCG  
TGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGAGCAGAG  
GCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACCGCTGTGGT  
CCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCTGATCCTGTCT  
GCGCTGGAGAGAGCCACCGTCTTCCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT  
GGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCGGGGAGAAGTGGGCCCAGGAGCCCCCTGC  
TGCAGCCGTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC  
CTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCAGCTGACCCTCCAGCCCGG  
GTTTTGGAAGCTCCCACATGCCTGGATCCACACTGATGCCTCCTTGGTGTACCCACGTTCTGGGC  
CCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGTGCAGCTGCTGGGAACCGGGACG  
GACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCCGGCTGCTC  
AGGCTACTGCCTGTCCCACCAACTGCTCTTCTTCTCTGGGCCAGAATGAGGGGATGCACACAGG  
GACCACTCCAACAGAGCCAGGACTATATCAACCTCTTCTGCGCCAACATGATGGACTTGAACCGC  
AGAGCTGAGGCCATCGGATACGCCTACCTTACCCGGGACATCTTCATGGAAAACATCATGTTCTG  
TGAATGGGCGGCTTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA  
AACAGCAGGAAGGATGCTTCGGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA  
TATCAGCAGCATTTTTTCGAGGAGAGTGAAGAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGT  
TGCTCAGGCTGGAGTACAGTGGCGCAATCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAAGC  
AATTCTCTTGCCTCATCCTCCCGAGTAGCTGGGACTACAGGAGCGTGCCACCATACCTGGCTAAT  
TTTTATATTTTTTTAGTAGAGACAGGGTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGAT  
CTCAAGAGATCCGCCCACCTCAGGCTCCCAAAGTGTGGGATTATAGGTGTGAGCCACCGTGTCTG  
GCTGAAAAGCACTTTCAAAGAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTC  
ATGGGGGCTCTCTCCCTAGATGGCTGCTCCTCCACAACACAGCCACAGCAGTGGCAGCCCTGG  
GTGGCTTCCTATACATCCTGGCAGAATACCCCCAGCAAACAGAGAGCCACACCCATCCACACCG  
CCACCACCAAGCAGCCGCTGAGACGGACGGTTCCATGCCAGCTGCCTGGAGGAGGAACAGACCCC  
TTTAGTCCTCATCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGG  
ATAAGCAAAGCCACCCCGACACCCAATCTTGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG  
GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAA

## **FIGURE 134**

MSARGRWEGGGRRACRGSGLLARAQGAERTVSSEQRPMASLGLLLLLLLLTALPPLWSSSLPGLD  
TAESKATIADLILSALERATVFLEQRLPEINLDGMVGVVRVLEEQLKSVREKWAQEPLLQPLSLRV  
GMLGEKLEAAIQRSLSLHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQDSFSEE  
RSDVCLVQLLGTGTDSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQGPLQSQD  
YINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILSWQKQEGCFG  
EPDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLPPGFKQFSLILP  
SSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRDPTSGSQSVGL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 39-56

**Tyrosine kinase phosphorylation sites.**

amino acids 149-156, 274-282

**N-myristoylation sites.**

amino acids 10-16, 20-26, 63-69, 208-214

**Amidation site.**

amino acids 10-14

**Glycoprotein hormones beta chain signature 1.**

amino acids 230-237

## FIGURE 135

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTG  
CTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCCGGGGCTGCTGCTGAGGGATCGGGAGG  
GAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGC  
CTCAGGACTGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAG  
ACAGATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGAAGTTGTATCTCC  
AGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCAAGATATG  
TGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATGAAATCTTCAGGT  
CCACCTTCTTACTTTATTAAAGGGAATCGTGGGGCTGGACAGACTTTCTAATGAACCCAATGGT  
TATGATGATGGTTCTTCTTTATTGATATTTGTGCTTCTGCCATAAGTGGTCAACACAAGTGATC  
CTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATTCACCATGAGTTGCCTGAT  
GTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAAATCATCTGGCAAATCTAGCAGCGGCAGCAG  
TAAACAGGCAAAAGTGGGGCTGGCAAAAGGAGGTAGTCAGGCCGTCCAGAGCTGGCATTGTCAC  
AAACACGGCAACACTGGGTGGCATCCAAGTCTTGAAAACCGTGTGAAGCAACTACTATAAACTT  
GAGTCATCCCGACGTTGATCTCTTACAACGTGTATGTT  
AACTTTTGTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTGTCTGTAT  
GAGGTCAATATTGATGTCAGTGAATTAATTACAGTGTCTATAGAAAATGCCATTAATAAATTAT  
ATGAACACTATACATTATGTATATTAATTAACATCTTAATCCAGAAATCAAAAAAAAAAAAAA  
AAAAAAAAAAAAAA

## **FIGURE 136**

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPDWISAA  
RVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSAPYRFDPVRVDITSKGKMRARYVNYIKTSE  
VVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMVLPLLIFVLLPKVVNTSDPDMRREME  
QSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTKSGAGKRR

### **Important features of the protein:**

#### **Signal sequence:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 161-182

#### **N-glycosylation site.**

amino acids 184-187

#### **Glycosaminoglycan attachment sites.**

amino acids 37-40, 236-239

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 151-154

#### **N-myristoylation sites.**

amino acids 33-38, 36-41, 38-44, 229-234

#### **Amidation site.**

amino acids 238-241

#### **ATP/GTP-binding site motif A (P-loop).**

amino acids 229-236

## FIGURE 137

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGGGA  
CCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATCCCCAAAACAA  
GTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTTCCAGGC  
CTTACCTGCTGGGCACCTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACGACCTGTGC  
CACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTTTCACGGGAGGCTTGGCAGT  
TTTTCTTACTCCTGTGGTCTCCAGATTTCAAGCCTAAGATGAAAGCCTCTAGTCTTGCCTTCAGC  
CTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAGACACTCAATTTGGG  
AAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGGCAGTG  
TGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAAGACACA  
AAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGACAGGGTATTTAA  
AAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTCGCCAATTCCTTTCTTA  
CCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACATGCCATTGTGGGGAGGAAGCAATG  
AAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGC  
TTTGGGGGAACTAGACATTCTTCTGCAATGGATGGAGGAGACAGAAATAGGAGGAAAGTGATGCTG  
CTGCTAAGAATATTTCGAGGTCAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAA  
ACCACCATCTCTTTACTGTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTG  
CTTCCTTGCAATGATTGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTT  
TGTAATATCTTTCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTGTCTATTTA  
ATGTATTTATTTTTTACTTGGACATGAACTTTAAAAAATTCACAGATTATATTTATAACCTG  
ACTAGAGCAGGTGATGTATTTTTATACAGTAAAAAATAACCTTGTAATCTAGAAGAGTGG  
CTAGGGGGGTATTCAATTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGAT  
ATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTGTGTGGAATTGCAC  
ATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATTAATTGTGTATCTTCCAG  
CCAGGAATCCTACAGGCCAGCATGTATTCTACAAATAAAGTTTCTTTGCATACCAAAAAA  
AAAAA

## **FIGURE 138**

MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNGATTTCATNSHSDSELRPEIF  
SSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG  
FSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKIS  
SLANSFLTIKKDLRLSHAHMTCHCGEAMKKYSQILSHFEKLEPQAQAVVKALGELDILLQWMEET  
E

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

## FIGURE 139

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCCGCATCCAGCC  
 TAGCGTGTCCACGATGCGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCGAGGTGC  
 TAGGGATCGCGGTCTTCTTCGCGGATTCTTCCCGGCTCCCGTTCGTTCCCTGCCAGAGCGGAA  
 CACGGAGCGGAGCCCCAGCGCCCCGAACCCTCGGCTGGAGCCAGTTCTAACTGGACCACGCTGCC  
 ACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAGATGATTTTGTGTTT  
 GGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTTACCTTGTGAAAAAGGAGCATCTCACAGT  
 TTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAATCAAGGCATTGATGACGGGGAG  
 CCTTCTGGCTTTGTGACGTCATCAGGAACCTCAATTCTCCTGCACTGCTGGAAGACAGTGTGA  
 TAAGACAAGCAAAGCAGCTGGAAGAAGATAGTCTTTTATGGAGATGAAACCTGGGTTAAATTA  
 TTCCCAAAGCATTGTTGGAATATGATGGAACAACCTCATTTCGTTGTCAGATTACACAGAGGT  
 GGATAATAATGTCACGAGGCATTGGAATAAGTATTAAGAGAGGAGATTGGGACATATTAATCC  
 TCCACTACCTGGGGCTGGACCACATTGGCCACATTTCAGGGCCCAACAGCCCCCTGATTGGGCAG  
 AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTGAAGGAGAGAGA  
 GACGCCTTTACCCAATTGCTGGTTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACG  
 GGGCCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTTAAATCAGTTCTGCGTTTGAAGGAAA  
 CCCGGTGATATCCGACATCCAAAGCAGTCCAATAGACGGATGTGGCTGCGACACTGGCGATAGC  
 ACTTGGCTTACCGATTCCAAAGACAGTGTAGGGAGCCTCCTATTCCAGTTGTGGAAGGAAGAC  
 CAATGAGAGAGCAGTTGAGATTTTACATTTGAATACAGTGCAGCTTAGTAACTGTTGCAAGAG  
 AATGTGCCGTATATGAAAAGATCCTGGGTTTGAGCAGTTTAAATGTCAGAAAGATTGCATGG  
 GAACCTGGATCAGACTGTACTTGGAGGAAAAGCATTGAGAAGTCTTATTCAACCTGGGCTCCAAGG  
 TTCTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCAG  
 TTCTCACCTGCTCCTGCTCAGCGTCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCA  
 CTGTCATCTCCTGGGTTTCTCTGCTCTTTTATTGGTGATCCTGGTTCTTTTCGGCCGTTACGCT  
 CATTGTGTGCACCTCAGCTGAAAGTTTCGTGCTACTTCTGTGGCCTCTCGTGGCTGGCGGACAGGCT  
 GCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGTGGCAGTGCCTGGAC  
 AGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCAGGCCTCTGGGTGTCCGACACAGGTG  
 TTCACATCTGTGCTGTGAGGTGAGTGCCTCAGTTCTTGAAAGCTAGGTTCTGCGACTGTTAC  
 CAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCCCCAGCTGAGGGGGTGTGTGAA  
 TCGGACAGCCTCCAGCAGAGGTGTGGGAGCTGCAGCTGAGGGAAGAAGAGACAATCGGCCTGGA  
 CACTCAGGAGGGTCAAAGGAGACTTGGTCGCACCACTCATCTGCCACCCCCAGAATGCATCCT  
 GCCTCATCAGGTCCAGATTTCTTTCAAGGCGGACGTTTCTGTTGGAATTTAGTCTTTGGCC  
 TCGGACACCTTCATTTCGTTAGCTGGGAGTGGTGGTGAGGCAGTGAAGAAGAGCGGATGGTCAC  
 ACTCAGATCCACAGAGCCCAGGATCAAGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCC  
 ACCCAACCTGCACAGCCCTCATCCCTCTTGGCTTGAGCCGTCAGAGGCCCTGTGCTGAGTGT  
 CTGACCGAGACACTCAGCTTTGTCATCAGGGCACAGGCTTCTCGGAGCCAGGATGATCTGTG  
 CCACGCTTGACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCTGCTATTGAATTAGTACCTAG  
 CTGCACACAGTATGTAGTTACCAAGAATAAACGGCAATAATTGAGAAAAAAA

## **FIGURE 140**

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGAEPPAPEPSAGASSNWTTLPPPLF  
SKVVIVLIDALRDDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF  
VDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWWKLFPHFVEYDGTTSFFVSDYTEVDNNV  
TRHLDKVLKRGDWDILILHYLGLDHHIGHISGPN SPLIGQKLSEMDSVLMKIHTSLQSKERETPLP  
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-34

#### **Transmembrane domain:**

amino acids 58-76

#### **N-glycosylation sites.**

amino acids 56-60, 194-198

#### **N-myristoylation sites.**

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,  
275-281, 278-284

#### **Amidation site.**

amino acids 154-158

#### **Cell attachment sequence.**

amino acids 205-208



## FIGURE 141

GGCACGAGGCAAGCCTTCCAGGTTATCGTGACGCACCTTGAAAGTCTGAGAGCTACTGCCCTACA  
GAAAGTTACTAGTGCCTTAAAGCTGGCGCTGGCACTGATGTTACTGCTGCTGTTGGAGTACAACT  
TCCCTATAGAAAACAACCTGCCAGCACCTTAAGACCACTCACACCTTCAGAGTGAAGAACTTAAAC  
CCGAAGAAATTCAGCATTTCATGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGGAATCTCAT  
AGCAGTTCCAGATAAAAACTACATACGCCCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCT  
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGGTCTCTAAAGGGGAGTTTTGTCTCTAC  
TGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAACTGATGAAGCT  
GGCTGCCCAAAGGAATCAGCACGCCGGCCCTTCATCTTTTATAGGGCTCAGGTGGGCTCCTGGA  
ACATGCTGGAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTGTAATGAGCCT  
GTTGGGGTGACAGATAAATTTGAGAACAGGAAACACATTGAATTTTCATTCAACCAGTTTGCAA  
AGCTGAAATGAGCCCCAGTGAGGTCAGCGATTAGGAAACTGCCCCATTGAACGCCTTCCTCGCTA  
ATTTGAACTAATTGTATAAAAACACCAAACCTGCTCACT

## **FIGURE 142**

MLLLLLLEYNFPIENNCQHLKTTHTFRVKNLNPKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEI  
FFALASSLSASAEGKSPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFI  
FYRAQVGSWNMLESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 33-36

N-myristoylation site.

amino acids 50-55, 87-92

Interleukin-1

amino acids 37-182

## FIGURE 143

CTAGAGAGTATAGGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTTTAA  
TCCAGGATCCTGTCTTCTGTCTGTAGGAGTGCTGTTGCCAGTGTGGGGTGAGACAAGTTTG  
TCCCACAGGGCTGTCTGAGCAGATAAGATTAAGGGCTGGGTCTGTGCTCAATTAACTCCTGTGGG  
CACGGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCTACAGTCAGCACCAATGCTGGGCCTGCCGTGG  
AAGGGAGGTCTGTCTGGGCGCTGTGCTGCTTCTCTTAGGCTCCCAGATCCTGCTGATCTATGC  
CTGGCATTTCACAGAGCAAAGGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA  
CAGTGGAGTTTGCTGTCCACACATTCAACCAACAGAGCAAGGACTACTATGCCTACAGACTGGGG  
CACATCTTGAATTCCTGGAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT  
GGGGAGAACTAGGTGTGGGAAATTTGAAGACGACATTGACAACCTGCCATTTCCAAGAAAGCACAG  
AGCTGAACAATACTTTACCTGCTTCTTCACCATCAGCACCAGGCCCTGGATGACTCAGTTCAGC  
CTCCTGAACAAGACCTGCTTGGAGGGATTCCACTGAGTGAAACCCACTCACAGGCTTGTCATGT  
GCTGCTCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTTCAGTGGCTGAGCAGCT  
TTGGACTTGTTTGTATCCTATTTTGCATGTGTTTGAGATCTCAGATCAGTGTTTTAGAAAATCC  
ACACATCTTGAGCCTAATCATGTAGTGTAGATCATTAACATCAGCATTTTAAGAAAAAAAAAA  
AAA

## **FIGURE 144**

MLGLPWKGGLSWALLLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY  
YAYRLGHILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQESTELNNTFTTCFFTISTRP  
WMTQFSLLNKTCLGFH

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 117-121, 139-143

N-myristoylation site.

amino acids 9-15

## FIGURE 145

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCGATGAGGAAG  
CACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGGTCCA  
GACGAGGGGCATCAAGCACAGAATCAAGTGGAACCGGAAGGCCCTGCCCAGCACTGCCCAGATCA  
CTGAGGCCCAGGTGGCTGAGAACCGCCCGGGAGCCTTCATCAAGCAAGGCCGAAGCTCGACATT  
GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCGATGGCATCCA  
CTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTCACCGGCTGCATCAATGCCA  
CCCAGGCGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACCAGCAGGTGCTCTGG  
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGGAGAGGGGCGCAGGACT  
TCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGATCTGGCTCATGGTGAAT  
AAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAATCCTGGCAAGTGACCCAGCT  
CTTCTCCCCCAAACCCACGCGTGTTCTGAAGGTGCCCAGGAGCGCGATGCACTCGCACTGCAAA  
TGCCGCTCCACGTATGCGCCCTGGTATGTGCCTGCGTTCTGATAGATGGGGGACTGTGGCTTCT  
CCGTCCTCCATTCTCAGCCCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT  
GAGAAGAACACATCAGGCACTGCGCCACCTGCTTCACAGTACTTCCCAACAACCTCTTAGAGGTAG  
GTGTATTCCCGTTTTACAGATAAGGAACTGAGGCCCAGAGAGCTGAAGTACTGCACCCAGCATC  
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCCTGGCTTGTCTAACCCAGGTTTTCTGCTCT  
GTCCAATTCCAGAGCTGTCTGGTGATCACTTTATGTCTCACAGGGACCCACATCCAAACATGTAT  
CTCTAATGAAATTGTGAAAGCTCCATGTTTAGAAATAAATGAAAACACCTGA

## **FIGURE 146**

MRKHLSSWWLATVCMLLFSHLSAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK  
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGTCINATQAANQGEFQKPDNKLHQQ  
VLWRLVQELCSIKHCEFWLERGAGLRVTMHQPVLLCLLALIWLMLVK

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

amino acids 157-171

#### **N-glycosylation sites.**

amino acids 98-102, 110-114

#### **Tyrosine kinase phosphorylation site.**

amino acids 76-83

#### **N-myristoylation sites.**

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

#### **Amidation site.**

amino acids 62-66

## **FIGURE 147**

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCATTT  
CCTGATGATTTATAGACTCAAAGAAAACTCATGTCAGAAGCTCTCTTCTCTTCTGGCCTCCTCT  
CTGTCTTCTTTCCCTCTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG  
AAATCTTTCATTTTGCTTGTCAGTGGGGTAGGTCAGTCTTAGTTTTATTTTTGAAATTT  
CAACTTTCAGATTCAGGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCATGATGCTGAGG  
TTTGGGGT

## **FIGURE 148**

MFRSSLLFWPPLCLLSLFLILISSIYSESKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE  
GLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

APP ID=10063534



## FIGURE 149

GTCTCCGCGTCACAGGAACTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGACTTGAC  
TCCCGCGCGCCCCAACCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCAGCCGCCAGTCC  
CGGCCCTCTCCGCCCCACCCACCCTCCTGGCTCTTCTGTTTTACTCCTCTTTTCATTGATA  
ACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCAAGCCGAGCGTGGAAGAATGGGGTT  
CCTCGGGACCGGCACTTGGATTCTGGTGTTAGTGCTCCCGATTCAAGCTTTCCCAACCTGGAGGAA  
GCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAA  
GCAGAAGAAGACAAGATTAAAAAACATATCCTCCAGAAAACAAGCCAGGTGAGAGCAACTATTCTTT  
TGTTGATAACTTGAACCTGCTAAAGGCAATAACAGAAAAGGAAAAATTGAGAAAAGAAACAATCTA  
TAAGAAGCTCCCCTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAACTG  
ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCA  
TCACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTATGAAG  
AAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAACTACTTAATCTCGGCCTTATCACAGAAAGC  
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCTCAAAGGAAGCCAACAA  
TTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAGGCTGAAAAATACCAGAGAAAG  
TGACTCCAATGGCAGCAATTCAGATGGTCTTGCTAAGGGAGAAAACGATGAAACAGTATCTAACACA  
TTAACCTTGACAAATGGCTTGAAAGGAGAACTAAACCTACAGTGAAGACAACCTTTGAGGAACTCCA  
ATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTGAGAAAAAGAACAAAAGAGAAAGAAA  
CACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCT  
CCAGAAGAAGGTGTTTCTACCTTGAAAACCTGGATGAAATGATTGCTCTTCAGACCAAAAACAAGCT  
AGAAAAAATGCTACTGACAAATATAAGCAAGCTTTTCCAGCACCATCAGAGAAGAGTCATGAAGAAA  
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAAA  
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGC  
CATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGAAGATTATGACCTTT  
CAAAGATGAGAGACTTCATCAATAACAAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAA  
GAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAATGGCAAAGATCCAGGAGTCTTTCAA  
CTGTTTCAGAAAACATAATATAGCTTAAACACTTCTAATCTGTGATTAAATTTTTTGACCCAAGG  
GTTATTAGAAAGTGCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAACATAGCTTTCTTCCC  
GTAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 150**

MGFLGTGTWILVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENKPG  
QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSGLDHK  
FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDEVAE  
VLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNTLTLTNGLE  
RRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISPEEGV  
SYLENLDEMIALQTKNKLEKNATDNISKLFPAPEKSHHEETDSTKEEAAKMEKEYGSLKDSTKDD  
NSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLKMRDFINKQADAYVEKGILDK  
EEAEAIAKRIYSSL

### **N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

### **Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390

### **N-myristoylation sites:**

amino acids 143-148, 239-244

## FIGURE 151

CGGCTCGAGGCTCCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCCTGTGGAGCTCAA  
**GATG**GTCTCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGC  
ATAATAACCAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTCAATAAGGTGAAGAGATCAGC  
GTGGTCCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCCGTCATCCTGGGTGTCCAGGGTGAAG  
CCAGTGCCGTGTCTGTGGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGG  
AGCTCTATCTTGGTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGCGGGACATGGGGCTCACC  
TCCAGCTTCGAGTCGGCTGCCTACCCGGGCTGGTTCTGTGCACGGTGCCTGAAGCCGATCAGCC  
TGTCAGACTCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCCATCACAGACTTCTACTTCC  
AGCAGTGTGACT**AG**GGCAACGTGCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAGGGGT  
GAGTGGAGGAGACCCATGGCGGACAATCACTCTCTGTCTCTCAGGACCCCCACGTCTGACTTAG  
TGGGCACCTGACCACCTTTGTCTTCTGGTTCAGTTTGGATAAAATCTGAGATTGGAGCTCAGT  
CCACGGTCCCTCCCCACTGGATGGTGTCTACTGCTGTGGAACCTTGTA AAAACCATGTGGGGTAAA  
CTGGGAATAACATGAAAAGATTTCTGTGGGGGTGGGGTGGGGGAGTGGTGGGAATCATTCTGTCT  
TAATGGTAAGTACAGAGTGTACCCCTGAGCCCCGAGGCCAACCCATCCCCAGTTGAGCCTTATA  
GGGTGAGTGTCTCCACATGAAGTCTGTCACTCACCCTGTGCAGGAGAGGGAGGTGGTCATA  
GAGTCAGGGATCTATGGCCCTTGGCCAGCCCCACCCCTTCCCTTAACTCTGCCACTGTCTATA  
TGCTACCTTTCTCTATCTTCCCTCATCATCTTGTGTGGGCATGAGGAGGTGGTGTATGTCTAGAA  
GAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCAA  
GATACAATCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAGTGTCTATGACATATTGAGA  
AGACCTACTTACAAAGTGGCATATATGCAATTTATTTTAAATTAAGATAACCTATTTATATATT  
TCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTGAGGGTGGTGGCAGTAT  
AGGTGATTTTTCTTTTAAATCTGTTAATTTATCTGTATTTCTTAATTTTTCTACAATGAAGATGA  
ATTCTCTGTATAAAAAATAAGAAAAGAAATTAATCTTGAGGTAAGCAGAGCAGACATCATCTCTGA  
TTGTCTCTCAGCCTCCACTTCCCCAGAGTAAATTCAAATTGAATCGAGCTCTGCTGCTCTGGTTGG  
TTGTAGTAGTGATCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGT  
GTGGCTGGAATCTCTGGGTAAAGAACTTAAAGAACAAAAATCATCTGGTAATTTCTTCTAGAAAG  
GATCACAGCCCCTGGGATTCCAAGGCATTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGA  
ATTGTGTCCCCCTCAAATTCACATCCTTCTTGGAACTCTCAGTCTGTGAGTTTATTTGGAGATAAG  
GTCTCTGCAGATGTAGTTAGTTAAGACAAGGTCTGCTGGATGAAGGTAGACCTAAATTCATAT  
GACTGGTTTTCTTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTA  
AAGATGAAGGCAGAGATCGGAGTTTTGCGAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACC  
ATCAGAAGCTTGGAAGAGGCAAAGAAGAATTCTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTG  
CTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAACGAAGAAAGATAAATTTTCGGCTGTTTTAA  
GCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAACTAATACAGCTGCTAAAATGATCCCTGT  
CTCCTCGTGTTTACATTTCTGTGTGTGTCCCTCCCAATGTACCAAAGTTGTCTTTGTGACCAA  
TAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATTAGGTATATAAAGACACTGCAGCTTC  
TACTTGAGCCCTCTCTCTCTGCCACCCACCGCCCCCAATCTATCTTGGCTCACTCGCTCTGGGG  
AAGCTAGCTGCCATGCTATGAGCAGGCCTATAAAGAGACTTACGTGGTAAAAATGAAGTCTCCT  
GCCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTT  
AAGTTGCTCAGTTTTGGTCTAACTTGTATGCAGCAATAGATAAAATAATATGCAGAGAAAGAG

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## **FIGURE 152**

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEESISVVPNRWLDASLSPVILGVQGG  
QCLSCGVGQEPTLTLEFPVNIMELYLGAKESKSTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP  
VRLTQLPENGGWNAPITDFYFQQCD

### **N-myristoylation sites.**

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

### **Interleukin-1 signature.**

amino acids 111-131

### **Interleukin-1 proteins.**

amino acids 8-29, 83-120, 95-134, 64-103

## FIGURE 153

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCCAGTTGCTCGAGTTAGAATTGTCTGCAATGCGCCGC  
CCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCCTGGCCACCAGCTGCCTCCTTCTCTTGG  
CCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAAC  
TTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA  
CAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT  
ATCTGATGAAGCAGGTGCTGAACCTCACCCCTGAAGAAGTGTGTTCCCTCAATCTGATAGGTTT  
CAGCCTTATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA  
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGC  
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAAGTGGATTGCTGTTTATGTCTCTGAGAAAT  
GCCTGCATTGACACAGAGCAAAGCTGAAAAATGAATAACTAACCCCTTTCCCTGCTAGAAATAA  
CAATTAGATGCCCCAAAGCGATTTTTTTTAAACAAAAGGAAGATGGGAAGCCAACTCCATCATG  
ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTTGTTTATA  
AGACCAGAAGGTAGACTTCTAAGCATAGATATTTATTGATAACATTTTCATTGTAAGTGGTGTTT  
TATACACAGAAAACAATTTATTTTTTAAATAATTGTCTTTTCCATAAAAAAGATTACTTTCCAT  
TCCTTTAGGGGAAAAAACCCCTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAA  
TGATTTTATTATTATTATAAGACTGCATTTTATTATATCATTTTATTAATATGGATTTATTTAT  
AGAAACATCATTCGATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTAT  
AGAGCTATAACATGTTTATTTGACCTCAATAAACACTTGGATATCCC

## **FIGURE 154**

MAALQKSVSSFLMGTIATSCLLLLLALLVQGGAAAPISSHCRLDKSNFQQPYITNRTFMLAKEASL  
ADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLFPQSDRFQPYMQEVVPFLARLSNRLS  
TCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

Important features of the protein:

Signal peptide:

amino acids 1-33

N-glycosylation sites.

amino acids 54-58, 68-72, 97-101

N-myristoylation sites.

amino acids 14-20, 82-88

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 10-21

## FIGURE 155

GGCTTGCTGAAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGT  
CAGTCAGTGCCCGACTTGTGACTGAGTGTGCAGTGCCAGCATGTACCAGGTCAGTGCAGAGGGC  
TGCTTGAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGC  
TGCCAGGTTTGGGGCTGGGGGCCAAGTGGAGTGAGAACTGGGATCCCAGGGGGAGGGTGCAGAT  
GAGGGAGCGACCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTTTCCTACAGGTGGTTGCAT  
TCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCCAGCTGCTGCCCCAGCAAAGGG  
CAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCCCTAGAGCCTGCTAG  
GCCCCAACCGCCACCCAGACTCCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGGCCATCT  
CCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCCAGGACCTGTACCACGCCCGT  
TGCCTGTGCCCCGACTGCGTCAGCCTACAGACAGGCTCCCACATGGACCCCCGGGGCAACTCGGA  
GCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCACCACA  
AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTGTGCGGCCCCGT  
GTGATGGGCTTAGCCGGACCTGCTGGAGGCTGGTCCCTTTTGGGAAACCTGGAGCCAGGTGTACA  
ACCACTTGCCATGAAGGGCCAGGATGCCCAGATGCTTGGCCCCCTGTGAAGTGTGTCTGGAGCAG  
CAGGATCCCCGGACAGGATGGGGGGCTTTGGGGAAAACCTGCACTTCTGCACATTTTGAAAAGAG  
CAGCTGCTGCTTAGGGCCCGCGAAGCTGGTGTCTGTCAATTTCTCTCAGGAAAGGTTTTCAAA  
GTTCTGCCCATTTCTGGAGGCCACCACTCCTGTCTCTTCTCTTTTCCCATCCCCTGCTACCCTG  
GCCAGCACAGGCACTTTCTAGATATTTCCCCCTTGCTGGAGAAGAAAGAGCCCTGGTTTTATT  
TGTTTGTCTTACTCATCTCAGTGAGCATCTACTTTGGGTGCATTCTAGTGTAGTTACTAGTCTT  
TTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATAGAGATTTATCCAAATAAATAT  
CTTTATTTAAAAATGAAAAA

## **FIGURE 156**

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHYSHWPSCCPSKGQDTSEELLRWSTVPVPPLEPA  
RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS  
ELLYHNQTVFYRRPCHGEKGTGTHKGYCLERRLYRVSLACVCVRPRVMG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-32

**N-glycosylation site.**

amino acids 136-140

**Tyrosine kinase phosphorylation site.**

amino acids 127-135

**N-myristoylation sites.**

amino acids 44-50, 150-156



## FIGURE 157

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCC  
GACCGTTCAATGTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCC  
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACAGTGTGCAACAGGGGACTATTCA  
ATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTGAAGGCCACCAA  
GATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTACAGCTGTGTGAGGTGCAATTACACAGAGG  
CCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCTTACATCGGCTTCCCTGTA  
GAGCTGAACACAGTCTATTTTATTGGGGCCATAATATTCTTAATGCAAATATGAATGAAGATGG  
CCCTTCCATGTCTGTGAATTTTACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAA  
AGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGTGAAGAAGATGAGGAGACA  
GTAGAAGTGAACCTTCAACAACACTCCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCAC  
TATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGA  
TTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTTACTTGTGGC  
AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCACAAACAGGCGTCCCTTTCCCTCT  
GGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCA  
CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTT  
TCTACCACCACACTACTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCA  
TCACACAATTTGTTACTTCACTGAATTTCTTCAAACCATTCGAGAAGTGAGGTCATCCTTGAAA  
AGTGGCAGAAAAAGAAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAGAAGGCA  
GCAGACAAAGTCGTCTTCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAA  
GAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCCTTTAACCTTTTCTGCA  
GTGATCTAAGAAGCCAGATTCTATCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACA  
AAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTT  
CTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACG  
ATGGCTGCTGCTCCTTGTAG

## **FIGURE 158**

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLPGLRDLRVEPVTTSVATGDYSILMNVSWV  
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFYSYIGFPVELNTVYFIGAHNIP  
NANMNEDGPSMSVNFTSPGCLDHIMYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQH  
STIIGFSQVFEPHQKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPTGVPFPLDNNK  
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFL  
QNHCRSEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLSNDVNSVCDGTGCKSEGSFSENSQDLFPLA  
ENLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELLHVKKQVSAGKRSQACHD  
GCCSL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-14

#### **Transmembrane domain:**

amino acids 290-309

#### **N-glycosylation sites.**

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283  
- 287

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

#### **Casein kinase II phosphorylation sites.**

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

#### **N-myristoylation site.**

amino acids 116-122

#### **Amidation site.**

amino acids 488-452

## FIGURE 159

AGCCACCAGCGCAACATGACAGTGAAGACCCTGCATGGCCCAGCCATGGTCAAGTACTTGCTGCT  
GTCGATATTGGGGCTTGCCTTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCAAAGTAGGACATA  
CTTTTTTCCAAAAGCCTGAGAGTTGCCCCGCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC  
ATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG  
GAATTACACTGTCACCTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCAAGTGTAGGA  
ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCCATCCAGCAA  
GAGACCCTGGTCGTCCGGAGGAAGCACCAAGGCTGCTCTGTTTCTTTCCAGTTGGAGAAGGTGCT  
GGTGACTGTTGGCTGCACCTGCGTCACCCCTGTCATCCACCATGTGCAGTTAAGAGGTGCATATCC  
ACTCAGCTGAAGAAG

## **FIGURE 16o**

MTVKTLHGPMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINEN  
QRVSMsrNIESRSTSPWNYTWTWDPNRYPSVVQAQCRNLGCINAQGKEDISMNSVPIQQETLVV  
RRKHQGCsvSFQLEKVLVTVGCTCVTPVIHHVQ

### **Signal sequence:**

amino acids 1-30

### **N-glycosylation site.**

amino acids 83-87

### **N-myristoylation sites.**

amino acids 106-111, 136-141

## FIGURE 161

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCAGG  
ACAGAGAGTGCACAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGGATTTC  
CAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGGCAGCAC  
AGGGCCTCAGGCCTGGGTGCCACCTGGCACCTAGAAGATGCCTGTGCCCTGGTTCTTGTGTCTCT  
TGGCACTGGGCCGAAGCCCAAGTGGTCTCTTCTCTGGAGAGGCTTGTGGGGCTCAGGACGCTACC  
CACTGCTCTCCGGGCTCTCTGCCGCTCTGGGACAGTGACATACTCTGCCTGCCTGGGGACAT  
CGTGCCCTGCTCCGGGCCCCGTGCTGGCGCTACGCACCTGCAGACAGAGCTGGTGTCTGAGGTGCC  
AGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCCACTTGGCCGTGCATGGGCACTGG  
GAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCTAGGAA  
TGCTCTCTCCAGGCCAAGTCTGCTCTCTCTCCAGGCCTACCCTACTGCCCGCTGCGTCTCTGC  
TGGAGGTGCAAGTGCCTGTCTGCCCTTGTGCACTTGGTCACTCTGTGGGCTCTGTGGTATATGAC  
TGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTCTTACTCAGCCCAGGTACGAGAA  
GGAATCAACCACACAGCAGCTGCCTGCCCTGCCCTGGCTCAACGTGTACGAGATGGTGACA  
ACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCACTTCGGCCTCTCCCTGTACTGGAATCAG  
GTCCAGGGCCCCCAAAACCCCGGTGGCACAAAACCTGACTGGACCGCAGATCATTACCTTGAA  
CCACACAGACCTGGTTCCTGCTCTGTATTCTAGGTGTGGCTCTGGAACCTGACTCCGTTAGGA  
CGAATCTGCCCCCTCAGGGAGGACCCCGCCACACCAGAACCTCTGGCAAGCCGCCGACTG  
CGACTGCTGACCTGCAGAGCTGGCTGCTGGACGCACCGTGTCTGCTGCCCGCAGAAGCGGCACT  
GTGCTGGCGGGCTCCGGGTGGGGACCCCTGCCAGCCACTGGTCCCACCGCTTCTCTGGGAGAACG  
TCACTGTGGACAAGGTTCTCGAGTTCCCATTTGCTGAAAGGCCACCCTAACCTCTGTGTTCAGGTG  
AACAGCTCGGAGAAGCTGCAGCTGCAGGAGTGTCTGTGGGCTGACTCCCTGGGGCCTCTCAAAGA  
CGATGTGCTACTGTTGGAGACACGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTTGGAAACCA  
GTGGCTGTACTTCACTACCCAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTACTA  
CAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTG  
CCCCATGGACAAATACATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTACTCTTTGCCG  
CTGCGCTTTCCCTCATCTCTCTCAAAAAGGATCACGCGAAAGGTGGCTGAGGCTCTTGAAA  
CAGGACGTCCGCTCGGGGGCGGGCCGAGGGGCCGCGCGGCTCTGCTCCTCTACTCAGCCGATGA  
CTCGGGTTTCGAGCGCTGGTGGGCGCCCTGGCGTGGGCCCTGTGCCAGCTGCCGCTGCCGCTGG  
CCGTAGACCTGTGGAGCCGTCTGTGAAGTACGCGCGCAGGGGCCGCTGGCTTGGTTTCACGCGCAG  
CGGCGCCAGACCTGCAGGAGGGCGCGTGGTGGTCTTGCTCTCTCTCCCGGTGCGGTGGCGCT  
GTGCAGCGAGTGGCTACAGGATGGGGTGTCCGGGCCCGGGCGCACGGCCCGCACGACGCTTCC  
GCGCTCGCTCAGCTGCGTGTGCCGACTTCTTGACGGGCCGGGCGCCCGGCAGCTACGTGGGG  
GCCTGTCTCGACAGGCTGCTCCACCGGACGCCGTACCCGCCCTTTTCCGCACCGTGCCGCTCTT  
CACACTGCCCTCCCAACTGCCAGACTTCTTGGGGGCCCTGCAGCAGCCTCGCGCCCCGCGTTCCG  
GGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCAGCCAGCCCTGGATAGCTACTTC  
CATCCCCGGGGACTCCCCGCGCGGACGCGGGGTGGGACCAGGGGCGGGACCTGGGGCGGGGA  
CGGGACTTAAATAAAGGCAGACGCTGTTTTTCTAAAAAA

## **FIGURE 162**

MPVPWFLLSLALGRSPVVLSELRLVGPQDATHCSPGLSCLWSDILCLPGDIVPAPGPFVLAPTHLQTELV  
LRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVLSTQAYPTARCVLLEV  
QVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSAADGNVHLVLNV  
EEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQ  
LWQAARLRLTLQSWLLDAPCSLPAEAALCWRAPGGDFCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQ  
VNSSEKLQLQECLWADSLGFLKDDVLLLETRGPQDNRSLEPSCGCTSLPSKASTRAARLGEYLLQDLQS  
GQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSILLKKDHAKGWLRLKQDVRSGAAARG  
RAALLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAVFWHAQRQTLEGGVVVLLFSP  
GAVALCSEWLQDGVSGFGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFT  
LPSQLPDFLGLAQPRAPRSRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domain.**

amino acids 453-475

### **N-glycosylation sites.**

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251,  
334-337, 357-360, 391-394

### **Glycosaminoglycan attachment site.**

amino acids 583-586

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 552-555

### **N-myristoylation sites.**

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617,  
692-697, 696-701, 700-705

## FIGURE 163

GGGAGGGCTCTGTGCCAGCCCCGATGAGGACGCTGCTGACCATCTTGACTGTGGGATCCCTGGCT  
 GCTCACGCCCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATCCAGTCCAGCAACTTTGA  
 AAACATCCTGACGTGGGACAGCGGGCCAGAGGGCACCCAGACACGGTCTACAGCATCGAGTATA  
 AGACGTACGGAGAGAGGGACTGGGTGGCAAAGAGGGCTGTGACGGATCACCCGGAAGTCCTGC  
 AACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTCACCGCT  
 GTCAGTGGGGAGGCCGGTCAGCCACCAAGATGACTGACAGGTTGAGCTCTCTGCAGCACACTAC  
 CCTCAAGCCACCTGATGTGACCTGTATCTCCAAAGTGAGATCGATTGAGATGATTGTTTCATCCTA  
 CCCCCACGCCAATCCGTGCAGGCGATGGCCACCGGCTAACCTGGAAGACATCTTCCATGACCTG  
 TTCTACCACTTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTTGGAGGGAAGCAGAGAGA  
 ATATGAGTTCTTCGGCCTGACCCCTGACACAGAGTTCTTGGCACCATCATGATTTGCGTTCCCA  
 CCTGGGCCAAGGAGAGTGCCCCCTACATGTGCCGAGTGAAGACACTGCCAGACCGGACATGGACC  
 TACTCCTTCTCCGGAGCCTTCTGTCTCCATGGGCTTCTCGTCGAGTACTCTGTACCTGAG  
 CTACAGATATGTACCAAGCCGCTGCACCTCCCACTCCCTGAACGTCCAGCGAGTCCCTGACTT  
 TCCAGCCGCTGCGCTTCATCCAGGAGCACGTCTGATCCCTGTCTTTGACCTCAGCGGCCCCAGC  
 AGTCTGGCCAGCCTGTCCAGTACTCCAGATCAGGGTGTCTGGACCCAGGGAGCCCGCAGGAGC  
 TCCACAGCGGCATAGCCTGTCCGAGATCACCTACTTAGGGCAGCCAGACATCTCCATCCTCCAGC  
 CCTCCAACTGCCACCTCCCCAGATCTCTCCCACTGTCTATGCCCAACGCTGCCCTGAG  
 GTCGGGCCCCCATCTATGCACCTCAGGTGACCCCCGAAGCTCAATTCCCATTTACGCCCCACA  
 GGCCATCTTAAGTCCAGCCTTCTCTATGCCCTCAAGCCACTCCGGACAGCTGGCCTCCCT  
 CCTATGGGTATGCATGGAAGTTCTGGCAAAGACTCCCCCACTGGGACACTTTCTAGTCTAAA  
 CACCTTAGGCCTAAAGGTCAGCTTCAGAAAGAGCCACCAGCTGGAAGCTGCATGTTAGGTGGCCT  
 TTCTCTGCAGGAGGTGACCTCCTTGGCTATGGAGGAATCCCAAGAAGCAAAATCATTGCACCAGC  
 CCCTGGGGATTTCACAGACAGAATCTGACCCAAATGTGCTACACAGTGGGAGGAAGGGACA  
 CCACAGTACCTAAAGGGCCAGCTCCCCCTCCTCTCCTCAGTCCAGATCGAGGGCCACCCCATGTC  
 CCTCCCTTTGCAACCTCCTTCCGGTCCATGTTCCCCCTCGGACCAAGGTCCAAGTCCCTGGGGCC  
 TGCTGGAGTCCCTTGTGTGTCCCAAGGATGAAGCCAAGAGCCAGCCCTGAGACCTCAGACCTG  
 GAGCAGCCACAGAACTGGATTCTCTTTTCAGAGGCTGGCCCTGACTGTGCAGTGGGAGTCCCTG  
 AGGGGAATGGGAAGGCTTGGTGCTTCTCCCTGTCCCTACCCAGTGTACATCCTTGGCTGTCA  
 ATCCCATGCCTGCCATGCCACACACTCTGCGATCTGCCTCAGACGGGTGCCCTTGAGAGAAGC  
 AGAGGGAGTGGCATGCAGGGCCCTGCCATGGGTGCGCTCCTCACCGGAACAAAGCAGCATGATA  
 AGGACTGCAGCGGGGGAGCTCTGGGGAGCAGCTTGTGTAGACAAGCGGTGCTCGCTGAGCCCTG  
 CAAGGCAGAAATGACAGTGCAAGGAGGAAATGCAGGGAACTCCCGAGGTCCAGAGCCCCACCTC  
 CTAACACCATGGATTCAAAGTGCTCAGGGAATTTGCCTCTCCTTGCCCCATTCTGGCCAGTTTC  
 ACAATCTAGCTCGACAGAGCATGAGGCCCTGCCTCTTCTGTCTATTGTTCAAAGGTGGGAAGAGA  
 GCCTGGAAAAGAACAGGCTGGAAAAGAACAGAGGAGGCTGGGCAGAACAGAACACCTGC  
 ACTTCTGCCAAGGCCAGGGCCAGCAGGACGGCAGGACTCTAGGGAGGGGTGTGGCTGCAGCTCA  
 TCCCCAGCCAGGGCAACTGCCTGACGTTGCACGATTTAGCTTCAATCCTCTGATAGAACAAAGC  
 GAAATGCAGGTCCACCAGGGAGGGAGACACAAAGCCTTTTCTGCAGGCAGGAGTTTCAGACCT  
 ATCCTGAGAATGGGGTTTGAAAGGAAGGTGAGGGCTGTGGCCCTGGACGGGTACAATAACACAC  
 TGTACTGATGTACAACCTTGCAAGCTCTGCCTTGGGTTAGCCCATCTGGGCTCAAATTCAGC  
 CTCACCACTCACAAGCTGTGTGACTTCAAACAAATGAAATCAGTGCCAGAACCTCGGTTTCTCT  
 ATCTGTAATGTGGGGATCATAACACCTACCTCATGGAGTTGTGGTGAAGATGAAATGAAGTCATG  
 TCTTTAAAGTGCTTAATAGTGCCTGGTACATGGGCAGTGCCCAATAAACGGTAGCTATTTAAAAA  
 AAAAAAA

## **FIGURE 164**

MRTLLTILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDTVYSIEYKTYGERDW  
VAKKGCQRITRKSCNLTVETGNLTLEYARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDVTCIS  
KVRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRTYQMHLGGKQREYEFFGLTPDT  
EFLGTIMICVPTWAKESAPYMCRVKTLPDRTWTYSFSGAFLESMGFLVAVLCYLSYRYVTKPPAP  
PNSLNQVRVLTFFQPLRFIQEHVLPVFDLSGPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT  
YLGQPDISILQPSNVPPPQILSPLSYAPNAAPEVGPPSYAPQVTPEAQFFPYAPQAISKVQPSSY  
APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPGQLQKEPPAGSCMLGGLSLQEVTSIAM  
EESQEAKSLHQPLGICTDRSDPNVLHSGEETPQYLKGQLPLLSSVQIEGHPMSLPLQPPSGPC  
SPSDQGPSPWGLLESIVCPKDEAKSPAPETSDLEQPTELDSLFRGLALTVQWES

### **Signal sequence.**

amino acids 1-17

### **Transmembrane domain.**

amino acids 233-250

### **N-glycosylation sites.**

amino acids 80-83, 87-90, 172-175

### **N-myristoylation sites.**

amino acids 11-16, 47-52, 102-107, 531-536, 565-570



## FIGURE 165

TGGCCTACTGGAAAAAAAAAAAAAAAAAAGTCACCCGGGCGCGGTGGCCACAACATGG  
CTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTCTGTCTGGGGGCGCTCTGGTGGGTCCCGGGCCAG  
TCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTGCAGCAT  
GTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGTGAATTTTA  
AAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAACCTTTGGGCTGGA  
AGTGTGTAACACAGTTTTGGATATTTTCCAAAAGATTTGATCAAGGTACTTCATAAATACACGGA  
AGAAGAGCTACATATTCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGGAGGAAGAGATGATT  
TTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAAGTGGAGGACTCTGTACCTGAAGAG  
TCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGAGGAGTCTCGGGGGCGTGA  
ACTTGACCCTGTGCCTGAGCCCGAGGCATTGAGAGCTGATTCAGAGGATGGAGAAGGTGCTTTCT  
CAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCTCACACCAGCGGT  
CCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACACTTTTGAAGAAATCTGCACGATAA  
ATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAGTTCTCCTGCCTCGGTGGAGCGGGAGA  
AGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGCCTTATT  
CATTACAGCAAAGGATTTGTTGGCATCAAATCTAAGTTTGTGTTTACAAAGATTGTTTTTAGTA  
CTAAGCTGCCTTGGCAGTTTGCATTTTGTAGCCAAACAAAATATATTATTTTCCCTTCTAAGTA  
AAAAAAAAAAAAAAAAAAAA

## **FIGURE 166**

MAAAPGLLFWLFWLGALWWVPGQSDLSHGRRFSDLKVCGDEEC SMLMYRGKALEDFTGPDCRFVN  
FKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEELHIPADETDFVCFEGGRD  
DFNSYNVEELLGSLELEDVPEESKKAEEV SQHREKSPEESRGRELDPVPEPEAFRA DSEDEGEA  
FSESTEGLQGQPSAQESH PHTSGPAANAQGVQSSLDTFEEILHDKLKVPGSESRTGNSSPASVER  
EKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNLSLFYKDCF

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 294-298

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34

Tyrosine kinase phosphorylation site.

amino acids 67-76

N-myristoylation sites.

amino acids 205-211, 225-231, 277-283

Amidation site.

amino acids 28-32

## FIGURE 167

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTGAGAGGCCGGGAAGAGAAGCAAAGCGC  
AACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCCTTAGGACATACACGGGACCCCTAACTTC  
AGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAACCTCAGCCCCGCACATCCACGCGCGGCACAGG  
CGCGGCAGCGCGCAGGTCCCAGGCCGAGGCGATGCGCGCAGGGGGTGGGGCAGCTGGGGCTCGGGC  
GGCGGGAGTAGGGCCCCGCGAGGGAGGCGAGGGAGGCTGCATATTCAGAGTCGCGGGCTGCGCCCTG  
GGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCCGCGATGAGCCGCGTGG  
TCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCCTTCTGCCGCGCGTGGTCAAGC  
GGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGGCCTACTTCCATGAACT  
GTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTTGTGAGAGTGAGGGAGGAGTCTCTCTCA  
GCCTTGAGAATGAAGCAGAACAGAAGTAAATAGAGAGCATGTTGCAAAACCTGACAAAACCCGGG  
ACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTGGAGGAATGGAGATGGGCAAACATCTGG  
TGCCTGCCCAGATCTCTACAGTGGTCTGATGGAAGCAATTCAGTACCGAACTGGTACACAG  
ATGAACCTTCCTGCGGAAGTGAAAAGTGTGTTGTGATGTATACCAACCAACTGCCAATCCTGGC  
CTTGGGGGTCCCTACCTTTACAGTGAATGATGACAGGTGTAACATGAAGCACAATTATATTTG  
CAAGTATGAACCAGAGATTAATCCAACAGCCCCGTAGAAAAGCCTTATCTTACAAATCAACCAG  
GAGACACCCATCAGAAATGTGGTTGTTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGT  
ATACCAACAATACCCCTGCTCTTACTGATACTGGTGTCTTTTGGAACTGTTGTTTCCAGATGCT  
GCATAAAAGTAAAGGAAGAACAAAACCTAGTCCAACACAGTCTACACTGTGGATTTCAAAGAGTA  
CCAGAAAAGAAAGTGGCATGGAAGTATAAATAACTCATTGACTTGGTCCAGAATTTTGTAATCT  
GGATCTGTATAAGGAATGGCATCAGAACAAATAGCTTGAATGGCTGAAATCACAAGGATCTGC  
AAGATGAACTGTAAGCTCCCCCTTGAGGCAAATATTAAGTAATTTTATATGTCTATTATTTC  
TTTAAAGAAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGTAAAGGATGCACCCAA  
ACTTCAAACCTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTA  
TGTGTGTAGAAGCAATTCCTTTTATTTCTTTTACCTTTTACATAAGTTGTTATCTAGTCAATGTAA  
TGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTGTTGATAAAA  
ATGAACCTGTTCTAATATTTATTTTATGGCATCTCATTTTCAATACATGCTCTTTTGATTAAAG  
AAACTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAGTTGT  
TTTCTCGAAATAATTCATCTTTTACAGTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTTCA  
AATAAGAAGCTATTTTCAATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGAT  
TGTCTAATTTCAATTTGTGCAAGACATGTGCCTTATAATTATTTTGTAGCTTAAATTAACAGATT  
TTGTAATAATGTAACCTTTGTTAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAG  
TGACATACACAATATAAATCATATGTCTTACACGTTGCCTATATAATGAGAAGCAGCTCTCTGA  
GGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTGCGGGGTTTGGG  
ATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTG  
ACTATATTAGTATACAAAGAGGTCTGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAG  
ACAAGCACAGCACACAGACATTTTAGGAAGGAAAGGAACACGAAATCGTGTGAAAATGGGTTGG  
AACCATCAGTGATCGCATATTCATTGATGAGGGTTTGCTTGAGATAGAAAATGGTGGCTCCTTT  
CTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCCTTGTCTTCTCAAGAGAAAGTTGTAACCTCT  
CTGGTCTTCATATGTCCTGTGCTCCTTTTAAACCAATAAAGAGTCTTGTCTTCTGGGGGAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 168**

MSRVVSLLLGAALLCGHGAFCRRVVSQKVCFADFKHPCYKMAYFHELSSRVSFQEARLACESE  
GGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDGFWIGLWRNGDGQTSACPDLYQWSDGSNSQ  
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNKYCKYEPEINPTAPVEK  
PYLTNQPGDTHQNVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSCKGRKTKTSPNQ  
STLWISKSTRKESGMEV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89, 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-  
145, 212-217